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US-08-346-128-34
US-08-532-384-13
US-08-893-828-34
US-08-537-210A-1
US-09-113-825-1
US-09-113-825-1
US-08-185-432-16
US-08-532-384-19
US-08-545-860D-55
PCT-US94-04496-55
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US-09-347-803-27
US-08-194-290-7
US-08-187-793-4
US-09-355-115-2
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RESULT	
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us-09-099-676 APPLICANT: Hillman, Jenniter L.
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE
TITLE OF INVENTION: HOMOLOG
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS: STREET: 3174 POI CITY: Palo Alto STATE: CA COUNTRY: US ZIP: 94304 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive , Applicatión 6100075 ØS/09099676

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/09/099,676
FILING DATE: HEREWITH
CLASSIFICATION UMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,

USA

INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids REGISTRATION NUMBER: 39,132
REFERENCE/OOCKET NUMBER: PFTELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555 STRANDEDNESS: TOPOLOGY: 111 TELEFAX: 650-855-0572 amino acid linear

; IMMEDIATE SOURCE: ; LIBRARY: PROSNO ; CLONE: 2278458 US-09-099-676-1 PROSNON01

US-09-565-910-3
US-08-665-716-2
US-08-665-150A-6
US-08-605-150A-1
US-08-605-150A-4
US-08-605-150A-4
US-08-752-929-17
US-08-752-929-17
US-08-752-929-17
US-08-605-150A-8
US-08-605-150A-10
US-08-605-150A-10
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US-08-804-227C-14 Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 17, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 14, Appli Sequence 14, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence

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                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 314 amino acid
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
OPERATING SYSTEM: Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE
                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                          NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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Patent No. 610007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: PROSNO
CLONE: 2278458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REBUCTASE
TITLE OF INVENTION: HOMOLOG
                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LDADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHALHFLE 240
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                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: HEREW
                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 POI
CITY: Palo Alto
                                                                                        NAME: Cerrone, Michael REGISTRATION NUMBER: 3
                                                                                                                                                FILING DATE:
                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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TELEX:
                 TELEFAX:
                                    TELEPHONE:
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                   650-855-0572
                                                                                                                                                                                                                                                                                                             IBM Compatible
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                                                                                                                                                                                                                      HEREWITH
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                                                                         PF-0532 US
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RESULT 4
US-09-565-910-3'
Sequence 3, Application
Fatent No. 6268192
FRERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennirer L.
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE
TITLE OF INVENTION: HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                  ATTORNEY/AGENT INFORMATION:
                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                       COMPUTER: IBM CONTROL OPERATING SYSTEM: SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                              STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                    FILING DATE:
                                                                                      CLASSIFICATION:
                                                                                                      APPLICATION NUMBER: US/09/565,910 FILING DATE:
                                                                                                                                                                                                                                              ZIP: 94304
                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDVLFLAVKPHIIPFILDEIGADIEDRHIVVSCAAGVTISSIEKKLSAFRPAPRVIRCMT 120
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Cerrone, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09565910
                                                                                                                                                                                                                                                                                                           3174 Porter Drive
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                                                                                                                                                                       Windows
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                                                  09/099,676
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                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                APPLICANT: REGISTER, ELIZABETH A
APPLICANT: MASCREKAR, PRAKASH S
TITLE OF INVENTION: P5C REDUCTASE GENE FROM ZALERION
TITLE OF INVENTION: ARBORICOLA
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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IMMEDIATE SOURCE:
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REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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LIBRARY: GENE...
189498
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                                                                                                                                                       COUNTRY: US
ZIP: 07065-0900
                                                                                                                                                                                                                   STREET: 126 E. LINCOLN AVENUE CITY: RAHWAY
                                                                                                                                                                                                                                                          ADDRESSEE: MERCK & CO., INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 84.1%; Score 1318; DB 4; Local Similarity 83.8%; Pred. No. 4.7e-136; Local Similarity 27; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LESGGFRSLLINAVEASCIRTRELQSMADQEQVSPAAIKKTILDKVKLDSPAGTALSPSG
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23-JUN-1995
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                                                       Release #1.0, Version #1.30
                US/08/665,716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-605-150A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 17, Application US/08605150A
Patent No. 6103520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KORSEN, ELLIOTT
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT\EP94\02936
FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hausmann, Ludger APPLICANT: Schell, Jozef TITLE OF INVENTION: GLYCEROI TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                            CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 TWIFKRIGDVVQLPAATMDASTALCGSGPAFFALILEAAIDGAVAMGLPRAEAQRMAAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 GVPAEQIYGYMYGKTPVNPEKEGLCQVVRAMPNTASGIRESMTVIATSSPPLSATTSSLI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 LLGAAKMLLDSEQHPCQLKDNVCSPGGATIHALHFLESGGFRSLLINAVEASCI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 900-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 18.8%; Score 294; DB 1; Length 304; Local Similarity 29.9%; Pred. No. 6.2e-24;
                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GVTISSVEKKLMAFQPAP------KVIRCMTNTPVVVQEGATVYATGTHAL-VEDGQLL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 KKALSPYKTPVKIIQSDNVTACREADVVLLGCKPYMAEGILGEEGMVDALKGKLLISILA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 -----KMGVNLTRSNKETV-KHSDVLFLAVKPHIIPFILDEIG-ADVQARHIVVSCAA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 LTLAVIGCGTMGIAILSGILASLDEIHAPNSQSSETDETPSKLPTKFIACVRSPKGAEKI 70
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                                                                                                   APPLICATION NUMBER: FILING DATE: 01-MAF
                                                                                                                                                                                                                                                                                                                                     CITY: Irvine
                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKGAAGLVLSGE-HPALLKDKVTTPGGCTIGGLMVLEEGGVRGTVARAVREATV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYAFMALDA--DGGVKMGLPRRLAIQLGAQA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88; Conservative
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                                                                                                UMBER: US/08/605,150A
01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCEROL-3-PHOSPHATE DEHYDROGENASE
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US-08-605-150A-6
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Best Local :
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
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FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Szekeres, Gabor L.
REGISTRATION NUMBER: 28,0
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LENGTH: 349 amino acid
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT\EP94\02936
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 GIPMSVLMGANI----ASEVAEEKFCETTIGCKDPAQGQLLKDLMQTPNFRITVVQEVDT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 EKEMLNGQKLQGP 300
                                                                                                APPLICATION NUMBER: FILING DATE: 01-MA
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les 59; Conserv
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Schell, Jozel
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                                                                                                  01-MAR-1996
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US-08-605-150A-4
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ATTORNEY/AGENT INFORMATION:
NAME: Szekeres, Gabor L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Topfer, Reinhard
APPLICANT: Hausmann, Ludger
APPLICANT: Schell, Jozef
TITLE OF INVENTION: GLYCEROL-3-PHOSPHATE DEHYDROGENASE
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
FILING DATE: 01-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT\EP94\02936
FILING DATE: 02-SEP-1994
                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,150A
FILING DATE: 01-MAR-1996
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klein & Szekeres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 EGPCMISSLISDLLG-----INCCVLNGANIANEIAVEKFSEATVGFRENRDIAEKWVQ 195
                                                                                                                                                                                                                                                                                                                                              STREET: 4199 (CITY: Irvine STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 RGQKLQGVSTAKEV----YEVLRHRGWLELFPLFSTVHEISTGRL 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 LGAAKMLLDSEQ-----HPCQLKD--NVCSPGGATIHALHFLESGGFRSLLINAVEASCI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 LFSTPYFMVSAVED----VEGVELCGTLKNIVAIAAGFVDGLEMGNNTKAAIMRIGLREM 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 542-04-PA
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Local Similarity 24.5%; Pred. No. 0.025;
hes 70; Conservative 51; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 AAGVTISSVEKKLMAFQPAPKVIRCMTNTPVVVQEGAT-VYATGTHALVEDGQLLE---Q 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 KLGRNVVADPDLENAVKDANML-VFVTPHOFVEGICKRLVGKIQEGAQALSLIKGMEVKM 141
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FILING DATE: 03-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 KMGVNLTRSN--KETVKHSDVLFLAVKPH-----IIPFILDEIGADVQARHIV----VSC 91
                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 92715
                                                                                                                                                                                                                                                                                                                                                                                             4199 Campus Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 714-854-4897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/08375709 Patent No. 5683898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
         ZIP: 2007-5109
ZIP: 2007-5109
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,709
FILING DATE: 20-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Szekeres, Gabor L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4329827.3
FILING DATE: 03-SEP-1993
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Gene Coding For Elcosapentaenoic Acid TITLE OF INVENTION: Synthesizing Enzymes and Process for TITLE OF INVENTION: Eiscosapentaenoic Acid
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 RGQKLQGVSTAKEV----YEVLRHRGWLELFPLFSTVHEISSGRL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 RTRELQSMADQEKISPAALKKTLLDRVKLE-SPTVSTLTPSSPGKL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 KAFSKLLFPSVKDTTFFESCGVADLITTCLGGRNRKVAEAFAKNGGNRS--FDDLEAEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 LGAAKMLLDSEQ-----HPCQLKD--NVCSPGGATIHALHFLESGGFRSLLINAVEASCI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 LMSSVGFCTEVEEDLIDAVTGLSGSGPAYAFMALDAD--GGVKMGLPRRLAI-QLGAQAL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 714-854-4897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 KMGVNLTRSN--KETVKHSDVLFLAVKPH-----IIPFILDEIGADVQARHIV----VSC 91
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                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
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CLASSIFICATION:
                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFSTPYFMVSAVED - - - - VEGVELCGTLKNIVAIAAGFVDGLEMGNNTKAAIMRIGLREM
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YAMADA, Akiko
KATO, Seishi
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24.5%; Pred. No. 0.026;
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FILING DATE: 14-MAY-PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:

14-MAY-1993

US 08/178,251

APPLICATION NUMBER:

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US-08-752-929-17
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                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08752929 Patent No. 5798259
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                  APPLICANT: KATO, Seishi
APPLICANT: KONDO, Kiyosi
TITLE OF INVENTION: Gene Coding for Eicosapentaenoic Acid Synthesizing
TITLE OF INVENTION: Enzymes and Process for Production of Eiscosapentaenoic
TITLE OF INVENTION: Acid
                                                                                                   NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 QVVKRGTLFPMRANKL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 ESPTVSTLTPSSPGKL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 PDAALATFINMGAAYIVTGSINQACVEAGASDHTRKILATTEMADVTMAPAADMFEMGVKL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 IHALHFLESGGFRSLLINAVEASCI-----RTRELQSMADQEKISPAALKKTLLDRVKL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 TDNRPLVTL------LPTILALKEEIQ-----AKYQYDT----PIRVG----CGGGVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 GPAYAFMALDADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 VIRCMINIPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 RTVEAS--AFLGLTPQIVYYRAAGLSRDAQGKVVVGNKVIAKVSRTEVAEKFM--MPAP- 233
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                                                           CJTY: Washington STATE: D.C.
                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 ETVKHSDVLFLAVKPHIIPFILDEIGADVQARHIVVS-CAAGVTISSVEKKLMAFQPAPK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                       20007-5109
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WEGNER, Harold C.
WEGNER, 125,258
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                                            USA
                                                                                                                                                                                                                                                                                        YAMADA, Akiko
                                                                                                                                                                                                                                                                                                         YAZAWA, Kazunaga
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                                                                                                      Suite 500
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                                                                                                                                                                                          US-09-090-793-10
                                                                                                                                                                                                                     RESULT
                   GENERAL INFORMATION:
APPLICANT: Calgene, LLC
APPLICANT: Calgene, LLC
TITLE OF INVENTION: Production of polyunsaturated fatty acids by expression
TITLE OF INVENTION: of polyketide-like synthesis genes in plants
FILE REFERENCE: CGNE.131.01US
                                                                                                                                           Sequence 10, Application US/09090793 Patent No. 6140486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.2%; Score 97.5; DB 1; Length 543; Best Local Similarity 22.5%; Pred. No. 0.053; Matches 71; Conservative 48; Mismatches 130; Indels 6
CURRENT APPLICATION NUMBER: US/09/090,793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-JAN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-MAY-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        373 QVVKRGTLFPMRANKL
                                                                                                                                                                                                                                                                                                                                        287 ESPTVSTLTPSSPGKL 302
                                                                                                                                                                                                                                                                                                                                                                                       313 PDAALATFNMGAAYIVTGSINQACVEAGASDHTRKLLATTEMADVTMAPAADMFEMGVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                 233 IHALHFLESGGFRSLLINAVEASCI-----RTRELQSMADQEKISPAALKKTLLDRVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 TDNRPLVTL-----LPTILALKEEIQ-----AKYQYDT---PIRVG---CGGGVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 GPAYAFMALDADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 VIRCMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 RTVEAS--AFLGLTPQIVYYRAAGLSRDAQGKVVVGNKVIAKVSRTEVAEKFM--MPAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 AGILCGSFGAAGLIPSRVEAAINRIQAALPNGPYMFNLIHSPSEPALERGSVELFLKHKV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 ETYKHSDYLFLAVKPHIIPFILDEIGADVQARHIVVS-CAAGYTISSVEKKLMAFQPAPK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 14-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 20-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WEGNER, Harol REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AGQLAYRFTAAGIL-----SAHKIIASSPE-----MNLPTVSALRXMGVNLTRSNK- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                           , 388
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; TYPE: PRT
; ORGANISM: Shewanella putrefaciens
US-09-090-793-10
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EARLIER APPLICATION NUMBER: 60/048,650
EARLIER FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3.5-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1+, ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CDNA FOR FANCONI ANEMIA COMPLEMENTATION GROUP NUMBER OF SEQUENCES: 18
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 38:
TELECOMMUNICATION INFORMATION:
                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hans Joenje, et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 GPAYAFMALDADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 VIRCMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGS 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 -----AKMLQKLVDDGSITAEQMELAQLVPMADDITAEADSG--GH 272
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                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 97204-2988
                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: 10/04/96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston, LLF STREET: One World Trade Center, Suite 1600, 121 S.W. Salmon
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5. 5952190
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                                                                                                                                                                                                                       US/08/726,012B
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                       3812-45520/RJP/DJE
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Best Local Similarity 22.3
79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (503) 228-9446 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT\EP94\02936
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4329827.3
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HAUSMANN, Ludger
APPLICANT: Schell, Jozef
TITLE OF INVENTION: GLYCEROL-3-PHOSPHATE DEHYDROGENASE
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 LDSMVTAFLVVRQAALEGPSAFLSYADWFKASFGSTRGYHGCSKKALVFLFTFLSELVPF 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 -----GQLLEQL------MSSVGFC-TEVEEDLIDAVTGLSGSGPAYAFMALD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 KKLMAFQPAPK-----VIRCMTNTPVV-----VQEGATVYATGTHALVED------ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 GIVSLQELLESHPDMHAVGSWLFRNL-CCLCEQMEASCQHADVARAMLSDFVQMFVLRGF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 ESPRYLQVHILHPPLVPSKYRSLLTDYISLAKTRLADLKVSIENMGLYEDLSSA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 -SPGGATIHALH-FLESGGFRSLLINAVEASCIRTREL----QSMADQEKISPA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDS-----EQHPCQLKDNVC------
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                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                STREET: 4199
CITY: Irvine
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                                                                                                                                 APPLICATION NUMBER: FILING DATE: 01-MAI
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                         Klein & Szekeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (503)
                                                                                                                                   01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                       Campus Drive,
03-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%; Score 95.5; DB 2; 22.3%; Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                     US/08/605,150A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                         Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                         700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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US-08-605-150A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                             COMPUTER READABLE FORM:
MEDING TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GLYCEROL-3-PHOSPHATE DEHYDROGENASE TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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LENGTH: 372 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 GOKLOGVSTAKEV----YEVLGHRGWLELFPLFSTVHEISTGRL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 TRELQSMADQEKISPAALKKTLLDRVKLE-SPTVSTLTPSSPGKL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 AFSKLLFPSVKDTTFFESCGVADLITTCLGGRNRKVAEAFAKNGGERS--FDDLEAELLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 GAAKMILDSEQ-----HPCQLKD--NVCSPGGATIHALHFLESGGFRSLLINAVEASCIR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 FSTPYFMVSAVED----VEGVELCGTLKNIVAIAAGFVDGLEMGNNTKAAIMRIGLREMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 MSSVGFCTEVEEDLIDAVTGLSGSGPAYAFMALDAD--GGVKNGLPRRLAI-QLGAQALL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 LISDLLG-----INC-----CVLMGANIANEIAVEKFSEATVGFRENTDIAEKWVQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 VEKKLMAFQPAPKVIRCMTNTPVVVQEGATV-----YATGTHALVEDGQLLE---QL 148
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
CLASSIFICATION: 800 RIGHT REPORT OF STREET STREET
                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 92715
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Irvine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 DPDLENAVKDANML-VFVTPHQFMEGICKRLVGKIQEGAQALSLIKGMEVKMEGPCMISS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 AAKLIASNTLKLPSFHDEVRMWVFEETLPSGEKLTDV-INQTNENVKYLPGIKLGRNVVA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AHKIIASSP------EMNLPTVSALRKMGVNLTRSN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 28 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KETVKHSDVLFLAVKPH-----IIPFILDEIGADVQARHIV----VSCAAGVTISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Klein & Szekeres
4199 Campus Drive,
                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hausmann, Lud
Schell, Jozef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Topfer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  714-854-4897
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                                                                     01-MAR-1996
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                                                                                                   US/08/605,1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542-04-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94.5; DB Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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INFORMATION FOR SEQ ID NO:
ZIP: UZLLU ZUC
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Smit, John
APPLICANT: Bingle, Wade H.
APPLICANT: NO. 597686461lini, John F.
APPLICANT: NO. 597686461lini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF
TITLE OF INVENTION: HETEROLOGOUS
TITLE OF INVENTION: POLYPEPTIDES FROM CAULOBACTI
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Szekeres, Gabor L.
REGISTRATION NUMBER: 28,
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                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & .... ADDRESSEET: 225 Franklin Street
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                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 ----KETVKHSDVLFLAVKPH-----IIPFILDEIGADVQARHIV----VSCAAGVTISS
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FILING DATE: 03-SEP-1993
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FILING DATE: 14 PARTICLE CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/895,367
FILING DATE: 09-JUNE-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: 435
REGISTRATION NUMBER: 08106/0020
REGISTRATION NUMBER: 08106/0020
REFERENCE/DOCKET NUMBER: 08106/0020
REFERENCE/DOCKET NUMBER: 08106/0020
REFERENCE/DOCKET NUMBER: 08106/0020
REFERENCE/DOCKET NUMBER: 08106/0020
RELECOMMUNICATION INFORMATION:
TELEPAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS:
FOPOLOGY: linear
MOLECULE TYPE: protein
US-08-614-377A-7
Search completed: January 31, 2002, 14:53:52 Job time: 22 sec
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                                                                                                                                                                                                                    928 DKLDLVGISTNGATADGAFGAAVTLGAAATL-----AQYLDAAAAGDGSGTSVAKWFQ 980
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OM protein - protein search, using sw model
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Run on: January 31, 2002, 14:54:15; Search time 12.98 Seconds (without alignments) 886.961 Million cell updates/sec

Title: Perfect score: US-09-912-717-1 1567

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table: Sequence: 1 MSVGFIGAGQLAYRFTAAGI......TPSSPGKLLTRSLALGGKKD 314

Total number of hits satisfying chosen parameters:

100059

100059 seqs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

3320987654	10 113 13 14 16 16 19 19 20 20 23	1 NO.	Result
179.5 163.5 109 104 104 102 102 102 102 101	326.5 326.5 323.5 306.5 306.5 301.5 297 297 281.5 281.5 281.5 2666 281.5 252.5	1306 512.5 501.5 501.5 479 476 476 421 402.5 377 377	2
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Query Match 83.3%; Score 1306; DB 1; Length 319; Best Local Similarity 82.7%; Pred. No. 1.5e-89; Matches 263; Conservative 27; Mismatches 22; Indels

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## ALIGNMENTS

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EMBL; M77836; AAA36407.1; PIR; A41770; A41770. MIM; 179035; InterPro; IPR000304; P5CR. Pfam; PF01089; P5CR; P5CR; PF01089; P5CR; PROSITE; PS00521; P5CR; 1. Oxidoreductase; Proline biosynthesis; NADP. SEQUENCE 319 AA; 33374 MW; F5E74B5BDFB475EF CRC64;	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE=92112831; PubMed=1730675;  Bougherty K.M., Brandriss M.C., Valle D.;  "Cloning human pyrroline-5-carboxylate reductase cDNA by complementation in Saccharomyces cerevisiae.";  J. Biol. Chem. 267:871-875(1992).  -i- CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = 1-PYRROLINE-5-CARBOXYLATE + NAD(P)H.  -i- PATHWAY: TERMINAL ("HIRD) STEP IN PROLINE BIOSYNTHESIS.  -i- SUBUNIT: HOMODECAMER OR HOMODODECAMER.  -i- SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE  FAMILY.		LT 1

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RA Huang E., Spiegel L., Gnoj L., Commercial T., Nelson J., Becker M., RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J., Becker M., RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M., RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Bante M., RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Dante M., RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M., RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P., RA Du H., Edwards J., Fryman J., Haakensen B., Riley A., Strowmatt C., RA Wagner M.CPherson C., Wollam A., Yoakum M., Bell M., Dedhia N., RA Warnerl L., Shah R., Rodriquez M., Hoon See L., Vil D., Baker J., RA Wirchoff K., Toth K., King L., Bahret A., Miller B., Marra M., Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T., RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I., RA Martienssen R., McCullagh B., Robben J., Grymonprez B., Zimmermann W., RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W., RA Wantseneger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., RA Pachgausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W., RA Behts O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H., Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.; P. Parker M., Martie P., Mewes H.-W., Bevan M., Fransz P.F.; P. Parker M., Martie P., Mewes H.-W., Bevan M., Fransz P.F.; P. Parker M., Martie P., Mewes H.-W., Bevan M., Fransz P.F.; P. Parker M., Martie P., Mewes H.-W., Bevan M., Fransz P.F.; P. Parker M., Martie P., Mewes H.-W., Bevan M., Fransz P.F.; P. Parker M., Martie P., Mewes H.-W., Bevan M., Fransz P.F.; P. Parker M., Martie P., Mewes H.-W., Bevan M., Fransz P.F.; P. Parker M., Martie P., Parker M., Martie P., Parker M., Parker M., Parker M., Martie P., Parker M., Pa
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MEDLINE-21016721; PubMed=11130714;
MEDLINE-21016721; PubMed=11130714;
Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E
Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
Kohara M., Matsumoto M., Matsuno S., Takeuchi C., Wada
Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada
Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston J.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston J.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston J.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
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01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C PROC1 OR AT5G14800 OR T913_100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verbruggen N., Villarroel R., Hua X., van Montagu M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE 94294559; PubMed 8022935;
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"Osmoregulation of a pyrroline-5-carboxylate reductase gene
Arabidonsis thaliana.":
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the Fithe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana.";
Nature 408:823-826(2000).
-i- CATALTIC ACTIVITY: L-PROLINE + NAD(P)(+) = 1-PYRROLINE-5-CARBOXYLATE + NAD(P)H.
CARBOXYLATE + NAD(P)H.
-i- PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.
"A soybean gene encoding delta 1-pyrroline-5-carboxylate reductase was isolated by functional complementation in Escherichia coll and found to be osmoregulated.";
                                                SEQUENCE FROM N.A.
MEDLINE=90340278; PubMed=2199815;
Delauney A.J., Verma D.P.S.;
                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; G
                                                                                                                                                                Eukaryota; Viridiplantae;
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Oxidoreductase; Proline biosynthesis; NADP.
SEQUENCE 276 AA; 28624 MW; B577A01C92A3A28B CRC64;
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                                                                                                                  NCBI_TaxID=3847,
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een the Swiss Institute of Bioinformatics
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42.5%;
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Pfam; PF01089; P5CR; 1.
PROSITE; P500521; P5CR; 1.
Oxidoreductase; Proline biosynthesis; NADP Coxidoreductase; Proline biosynthesis; NADP SEQUENCE 274 AA; 28586 MW; 933CFCFDD755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    Q04708;
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X16352; CAA34401.1; -. PIR; S10186; S10186.
                            Williamson C.L., Slocum R.D.;
"Molecular cloning and evidence for osmoregulation pyrruline-5-carboxylate reductase (proC) gene in population
                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisu
Plant Physiol. 100:1464-1470(1992)
                                                                                  SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=3888;
                                                                                                                                                                                     Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCM 117
                                                                                                                                                                                                                                                                                                                                                                                               IHELENGGFRGTLMNAVVAAAKRSREL
                                                                                                                                                                                                                                                                                                                                                                                                                               LHFLESGGFRSLLINAVEASCIRTREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLAIEALADGGVAAGLPRDLSLSLASQTVLGAASMVSQTGKHPGQLKDDVTSPGGTTITG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNTPAAVGQAASVMSLGGSATEEDGNIIAQLFGSIGKIWKAEEKYFDAITGLSGSGPAYV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESDVVVL9VKPQLVKDVVSKLTPLLTKHKLLVSVAAGTKL----KDLQEWAGNDRFIRVM
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YTIC ACTIVITY: L-PROLINE + NAD(P)(+) - 1-PYRROLINE-5-
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Pred. No. 3.1e-30;
                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                              273 AA
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pfam; pF01089; P5CR; 1.
pROSITE; P5CB; 1.
Oxidoreductase; Proline biosynthesis; NADP.
SEQUENCE 273 AA; 28237 MW; D719F5293596
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Actinidiaceae; Actinidia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
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                     TISSUE=Axillary bud;
Walton E.F., Podivinsky E., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.P. Walton E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Reynolds P.H.S., Young L.Walton E.F., Podivinsky E.F., Wu R.M., Podivinsky E.F., Podivinsky E.F., Wu R.M., Podivinsky E.F., Podivins
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3625;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinidia chinensis (Kiwi) (Yangtao)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AGVHELEKGGFRGTLMNAVVAAAKRSREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 HALHFLESGGFRSLLINAVEASCIRTREL 262
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                                                         TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
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Pred. No. 1.4e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
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                                                                                                                                            Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROC_SYNY3
P74572;
15-JUL-1998
                      This
                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (BC 1.5.1.2)
                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                          Synechocystis sp. (strain Bacteria; Cyanobacteria; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNY3
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OXIDOR DESCRIPTION OXIDERATE: NADE.

OXIDENCE 278 AA; 29003 MW; 198B6E934F190236 CRC64;
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                 Res. 3:109-136(1996).

CAPALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = 1-PYRROLINI
CARBOXYLATE + NAD(P)H.

CARBOXYLATE + NAD(P)H.

PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS
SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDI
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Duncan M., Federspiel

Allen E., N., Hyman

Araujo

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Aparicio S., Komp

C., K

Kurdi O.,

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Davis

Kalman

SEQUENCE FROM N.A

Science

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K-12.";

Mau B.,

Shao Y.;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

STRAIN=K12 / MG1655; MEDLINE=97426617; PubMed=9278503;

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A ACCORDANCE OF THE PROPERTY O
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Best Local
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARLING SEQUENCE FROM N.A., AND PARLING SEQUENCE FROM N.A., AND PARLING SEQUENCE 116986; PubMed=6296787;

MEDLINE=83116986; PubMed=6296787;

Deutch A.H., Smith C.J., Rushlow K.E., Kretschmer P.J.;

"Escherichia coli delta 1-pyrroline-5-carboxylate reductase: gene sequence, protein overproduction and purification.";

sequence, protein overproduction and purification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROC_ECOLI P00373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-JUG-2001 (Rel. 40, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
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Best Local S
Matches 98
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MEDLINE-90185238; PubMed-2107123;
Savioz A., Jeenes D.J., Kocher H.P., Haas D.;
"Comparison of proC and other housekeeping genes of
                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1
                                                                                                                                                                                                                                PROC_PSEAE P22008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EcoGene; EGI0769; proC.
InterPro; IPR000304; P5CR:
Pfam; PF01089; P5CR; 1.
PROSITE; PS00521; P5CR; 1.
Oxidoreductase; Proline biosynthesis; NADP; Complete SEQUENCE 269 AA; 28145 MW; C5E2CED36BCC508D CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutens as long as its content is in entitles requires a license agreement. Usage to send an email -- .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W., Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

1. CATALYTIC ACTIVITY: L-POLINE + NAD(P)(+) = 1-PYRROLINE-5-CARBOXYLATE + NAD(P)H.

1. PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000145; AAC73489.1; -.
EMBL; U7385; AAB18110.1; -.
PIR; A00385; RDECC.
HSSP; P14295; 1HYH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                  SEQUENCE
                                                                                                                                       Pseudomonas aeruginosa
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                                                                                                                                                         OR PA0393.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADIIFAAVKPGIMIKVLSEITSSLNKDSLVVSIAAGVTLDQLAR---ALGHDRKIIRAMP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGFIGAGQLAYRFTAAGILSAHKIIASSPEMNLPT---VSALR-KMGVNLTRSNKETVKH 58
                                                                                                                                                                                                                                                                                                                                                                                  MFIEAMADAAVLGGMPRAQAYKFAAQAVMGSAKMVLETGEHPGALKDMVCSPGGTTIEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                           NTPALVNAGMTSVTPNALVTPEDTADVLNIFRCFGEAEVIAEPMIHPVVGVSGSSPAYVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGFIGCGNMG-KAILGGLIASGQVLPGQIWVYTPSPDKVAALHDQFGINAAESAQEVAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J01665; AAA86433.1; -.
                                                FROM N.A., AND S
TCC 15692 / PAO1;
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                                                                                                                                                                                                                                               STANDARD;
                                                               AND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.7%;
35.5%;
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Pred. No. 6.
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                                                                                                                                                                    (P5CR) (P5C REDUCTASE).
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   Pseudomonas
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Oxidoreductase; Proline biosynthesis; NADP; Complete proteome
INIT_MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Bridy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lin R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M33557; AAA25975.1; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = 1-PYRROLINE-5-CARBOXYLATE + NAD(P)H.
-i- PATHHAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.
-i- SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 101:33-44(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000304; P5CR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitchurch C.B., Hobbs M., Livingston S.P., Krishnapillai V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 15692 / PAO1;
MEDLINE=91285432; PubMed=1676385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-6 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterisation of a Pseudomonas aeruginosa twitching motility
               233 IHALHFLESGGFRSLLINAVEASCIRTRELQSMADQ
                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                     3 VGFIGAGQLAYR----FTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JQ0418; JQ0418.
                                                   AYFFLLMQAMTDAGEKLGLSRETASRLTLQTALGAAQMALSSEVEPAELRRRVTSPNGTT
                                                                                         AYAFMALDA--DGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGAT
                                                                                                                                                                 NTPVVVQEGAT-VYATGTHALVEDGQLLE--QLMSSVGFCTEVEEDL-IDAVTGLSGSGP
                                                                                                                                                                                                       ADVVVLSVKPQAMKAVCQALAPALKPEQLIVSIAAGIPCASLEAWL--GQPRP-VVRCMP
                                                                                                                                                                                                                                             SDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMT 118
                                                                                                                                                                                                                                                                                 IAFIGAGNMAASLIGGLRAQGVPAA-QIRASDPGAE-QRAKIAGEFAIDVVESNAEAVAD
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                                                                                                                             NTPALLRQGASGLYA----NAQVSAAQCEQAGQLLSAVGIALWLDDEAQIDAVTAVSGSGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 AA;
                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                              24.1%;
36.6%;
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Pred. No. 4.8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                              Length 272;
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237 EAAIKSFQANGFEALVEQALNAASQRSAELAEQLGQ 272

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ankri S., Serebrijski I., Reyes O., Leblon G.;

"Mutations in the Corynebacterium glutamicum proline biosynthetic
pathway: a natural bypass of the proA step.";

J. Bacteriol. 178:4412-4419(1996).

-!- CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = 1-PYRROLINE-5-
CARBOXYLATE + NAD(P)H.

-!- DATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.

-!- SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00521; P5CR; 1.
Oxidoreductase; Proline biosynthesis; NADP
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NCBI_TaxID=1718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P46540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                               116 ---VVRVMPNTPMLVGKGMSTVTKGRYVDAEQLEQVKDLLSTVGDVLEVAESDIDAVTAM
243
                                                                       228 PGGATIHALHFLESGGFRSLLINAVEASCIRTREL 262
                                                                                                                                                                                                           170 SGSGPAYAFMALDA--DGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCS
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                                                                                                                                                                                                                                                                                                                                                                                                                   SQAADEADVVFLCVKPKFIVEVLSEITGTLDNNSAQSVVVSMAAGISIAAMEESASAGLP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KETVKHSDVLFLAVKPHIIPFILDEIGADV---QARHIVVSCAAGVTISSVEKKLMAFQP 109
   PAGTTVAAIRELEESGIRGAFYRAAQACADRSEEL
                                                                                                                                           SGSSPAYLFLYTEALIEAGVNLGLPRATAKKLAVASFEGAATMMKETGKEPSELRAGVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 370; DB 1;
Pred. No. 1.6e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90150E233D94158F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
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                                                                                                                                                                                                                                                                                  172
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RESULT

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w

VGFIGAGQLAYRFTAAGILSAHKI----IASSPEMNLPTVSALR-KMGVNLTRSNKETVK 57

:: :: ::

Matches Best

Local

88; Conser

Conservative

53;

Score 345; DB 1; Pred. No. 1.1e-18; 3; Mismatches 101

101;

Indels 12;

Gaps

6

Length 270

22.0%;

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reprication terminus of Bacillus subtilis 168 and W23 chromos Gene 98:107-112(1991).
                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified
                                                                                                                                                                                                                                                                                                                                                                                                         "DNA and protein sequence conservation at the replication terminus Bacilius subtilis 168 and W23.";
J. Bacteriol. 171:1402-1408(1989).
-i- FUNCTION: NOT KNOWN, BUT COULD BE INVOLVED IN GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunst F., Ogasawara N.,
Submitted (NOV-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P14383; 031828;
01-JAW-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                         Pfam; PF01089; P5CR; 1. PROSITE; PS00521; P5CR; 1
                                                                                                                                                                                               SubtiList; BG11049; yoxE
                                                                                                                                                                                                                        EMBL; M24523; AAA22722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89155440; PubMed=2493444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis
SEQUENCE
                                     VARIANT
                                                   VARIANT
                                                               VARIANT
                                                                                          VARIANT
                                                                                                        VARIANT
                                                                                                                    VARIANT
                                                                                                                               Hypothetical VARIANT
                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              entities requires a
                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-W23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-200 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-W23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-256 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YOXE OR PROC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRROLINE-5-CARBOXYLATE REDUCTASE HOMOLOG
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            CONFLICT
                        VARIANT
                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lewis P.J., Wake R.G.;
                                                                                                                                                                                  InterPro; IPR000304; P5CR.
                                                                                                                                                                                                                                                                                                                                                                       FAMILY
                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS
                                                                                                                                                                                                             в32807; в32807.
                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .S., Wake R.G
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND 168;
                                                                                                                 . protein;
58 51
70 70
ΑĀ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1849493;
            58
70
74
93
100
127
159
236
239
                                                                                                                                                                                                                                                                              license agreement (See http://www.isb-sib.ch/announce/
29402 MW;
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                                                                                                                                              Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ
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        Dreductase; Complete proteome.

T -> A (IN STRAIN W23).
L -> S (IN STRAIN W23).
L -> I (IN STRAIN W23).
L -> I (IN STRAIN W23).
S -> T (IN STRAIN W23).
S -> T (IN STRAIN W23).
E -> Q (IN STRAIN W23).
E -> Q (IN STRAIN W23).
H -> Q (IN STRAIN W23).
H -> Q (IN STRAIN W23).
I -> V (IN STRAIN W23).
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C7B9E1680B7FF9A7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Danchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and W23 chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.;
databases.
 CRC64;
                                                                                                                                                                                                                                                                                            commercial
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RESULT
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PROSITE; PS00521; P5CR; 1.
Oxidoreductase; Proline biosynthesis; NADP; Complete proteome.
SEQUENCE 294 AA; 30237 MW; EA8608C9CBBB6D9D CRC64;
                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                     EMBL; U00018; AAA17233.1; -. EMBL; AL583925; CAC31947.1; -. Leproma; ML2430; -.
                                                                                                                                                                                                                                                                                                                                                                        "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).

-I- CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = 1-PYRROLINE-5-
CARBOXYLATE + NAD(P)H.

-I- PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P46725;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
PROC OR ML4430 OR B2168_C2_211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Squares S., S
Barrell B.G.;
                                                                 Pfam; PF01089; P5CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wEDLINE-21128732; PubMed-11234002;
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                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DMDVLILAMKPKDAENALSSLKSRIQPHQLILSVLAGITTSFIEQSLLNEQP---VVRVM 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Robison K.; (MAR-1994) to
                                                                                   IPR000304; P5CR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268
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                   Query Match
Best Local :
    Matches
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01-OCT-1996
20-AUG-2001
                                                                                                                                                                                       EMBL;
                                                                         Hypothetical protein; Oxidoreductase; Complete proteome. SEQUENCE 278 AA; 30396 MW; 4B69DB527E55345E CRC64;
                                                                                                        Pfam; PF01089; P5CR; 1. PROSITE; PS00521; P5CR; 1.
                                                                                                                                       Subtilist; BG11744; yqjo.
InterPro; IPR000304; P5CR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE HOMOLOG 2
                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                     Kobayashi Y., Mizuno M., Masuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
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P54552;
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168 / JH642;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRHSAEVAPLGAQVDVPAAQLRATITSPGGTTAAALRELERGGLRMVVDAAVQAAKIRSE
                                                                                                                                                                       D84432; BAA12621.1; -. 299116; CAB14312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESQMDAVTAVSGSGPAYFFLLVEALVDAGVAVGLTRQVATELAAQTMAGSAAMLLERMDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLMAFQPAPKVIRCMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMS---SVGFCTEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; Conser
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Takeuchi M.;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
              20.7%; Score 324.5; DB 1; 29.9%; Pred. No. 3.7e-17;
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 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 326.5; DB
Pred. No. 2.8e-17
 Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Takemaru K., Hosono S.,
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                                                                                                                                                                                                                                                                                                                                                                         databases
                             Length
 Indels 39;
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                                                                                                                                                                                                                                                                                                                                                         REDUCTASE
Gaps
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3 VGFIGAGQLAYR----FTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETVKH 58

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"Molecular cloning and sequence analysis of the proC gene encoding delta 1-pyrroline-5-carboxylate reductase from an extremely thermophilic eubacterium Thermus thermophilus.";
Biochem. Blophys. Res. Commun. 199:410-417(1994).
-!- CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = 1-PYRROLINE-5-
                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1999 (Rel. 38, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
                                                                                                                                                                                                        Pram; PFUJU89; P5CR; 1.

PROSITE; PS00521; P5CR; 1.

Oxidoreductase; Proline biosynthesis; NADP.

SEQUENCE 261 AA; 27819 MW; 3435C3A8F4299B3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94168609; PubMed=8123043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermus aquaticus (subsp. thermophilus)
                                                                                                                                                                                                                                                                                                     EMBL; D25413; BAA05001.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
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 54
                                 乜
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOXYLATE + NAD(P)H.
PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITSPGGTTEAGLRALQDSRFEEAIIHCIEETAKRSAEI-----KEQFAGAALER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCSPGGATIHALHFLESGGFRSLLINAVEASCIRTRELQSMADQEKISPAALKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAIAGSGPAYVYRYIEAMEKAAQKVGLDKETAKALILQTMAGATDMLLQSGKQPEKLRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGLSGSGPAYAFMALDA--DGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AVIRVMPNTSAAIRKSATGFSVSTEASKNDIIAAKALLETIGDATLVEERHLDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQPAPKVIRCMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDIIILAFKPKDAAESIDSIRPYIKDQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDVLFLAVKP-----HIIPFILDEIGADVQARHIVVSCAAGVTISSVE----KKLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGFYGAGSMAEAMINGILQSGITKPEHIYITNRSNDERLIELKETYSVRPCRDKNEFFTH
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   ETVKHSDVLFLAVKPHIIPFILDEIGADVQARHIV--VSCAAGVTISSVEKKLMAFQPAP 111
                                      MRLAFVGLGKMGRSILKGALERGFLRPEEVGVLGRTPERSR---ELAEPFGVRPLTRAD-
                                                                         MSVGFIGAGQLAYRFTAA----GILSAHK--IIASSPEMNLPTVSALRKMGVN-LTRSNK 53
                                                                                                                                                                                                                                                                  PF01089;
                                                                                                                93;
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus/Deinococcus group; Thermus group; Thermus
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1089; P5CR; 1.
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(Rel.
(Rel.
                                                                                                                Conservative
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34,
                                                                                                                                    20.6%;
                                                                                                                45;
                                                                                                                                    Pred. No. 4.1e-17;
                                                                                                                                                   Score 323.5;
                                                                                                                  Mismatches
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                                                                                                                                                   DB 1;
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                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL outstation
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                                                                                                                  29;
                                                                                                                Gaps
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harricordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyc Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
20-ANG-2001 (Rel. 40, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCTU
                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98295987; PubMed=9634230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROC OR RV0500 OR MT0520 OR MTCY20G9.26
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                               laboratory strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSGPAYAFMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSP
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or send an email to license@isb-sib.ch).

Z77162; CAB00926.1; AE006952; AAK44743.1;

TubercuList; TIGR; MT0520;

IPR000304;

P5CR

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PROC_NEUCR
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Best Local 9
EMBL; U30317; AAA83568.1; -.
InterPro; IFR000304; P5CR.
Pfam; PF01089; P5CR; 1.
PROSITE; PS00521; P5CR; 1.
Oxidoreductase; Proline biosynthesis; NADP.
Oxidoreductase; Proline biosynthesis; NADP.
                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     Davis C.R., McPeek M.A., McClung C.R., Molecular characterization of the proline-1 (pro-1) locus of Neurospora crassa, which encodes delta 1-pyrroline-5-carboxylate
                                                                                                                                                                                                                                                                                                MO1. Gen. Genet. 248:341-350(1995).
-I- CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = 1-PYRROLINE-5-CARBOXYLATE + NAD(P)H.
-I- PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.
Reukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                   reductase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96004701; PubMed-7565596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q12641;
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Oxidoreductase; Proline biosynthesis; NADP; Complete proteome.
SEQUENCE 295 AA; 30171 MW; F95C3F407BE5408F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01089; P5CR; 1. PROSITE; PS00521; P5CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 KSRSEQLRITP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 QSMADQEKISP 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 ------PCQLKDNVCSPGGATIHALHFLESGGFRSLLINAVEASCIRTREL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 QLDAVTAVSGSGPAYFFLLVEALVDAGVGVGLSRQVATDLAAQTMAGSAAMLLERMEQDQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 LIDAVTGLSGSGPAYAFMALDA--DGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQH-- 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 SKLPAGTP----VVRAMPNAAALVGAGVTALAKGRFVTPQQLEEVSALFDAVGGVLTVPES 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 KKLMAFQPAPKVIRCMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEED 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 LYTSAADAVENATFYVVAVKPADVEPVIADLANATAAAENDSAEQVFYTVVAGITIAYFE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 LTRSNKETVKHSDVLFLAVKP-HIIPFILDEIGADV-----QARHIVVSCAAGVTISSVE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91; Indels 35;
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                                                                           220 ADGGVAMGLPRAEANRMAAQTMRGAAGLVLEGE-HPAILREKVSTPGGCTIGGLLVLEEG
279 GVRAAVARAVREATV 293
                                         243 GFRSLLINAVEASCI 257
                                                                                                                  183 ADGGYKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHALHFLESG
                                                                                                                                                                                         160
                                                                                                                                                                                                               126 EGATYYATGTHALVED-GOLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYAFMALD-- 182
                                                                                                                                                                                                                                                             100 DALTVKHTEGHARSQKIIISICAGVTVPDLERVLREDVGLSADNLPIVVRAMPNTASKIR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 19.2%; Score 301.5; DB 1; Length 311;
Local Similarity 31.8%; Pred. No. 2.1e-15;
hes 81; Conservative 49; Mismatches 102; Indels 23
                                                                                                                                                                                                                                                                                                                             08
                                                                                                                                                                                                                                                                                                                                                     43 SVAKVESALSPLVKPSVSTLR----VLQSTSNVSAAAEADIILLGCKPYMVSGLLSASGMK 99
                                                                                                                                                                                                                                                                                                                                                                                              22 SAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETVKHSDVLFLAVKPHIIPFILDEIG-- 79
                                                                                                                                                                   ESMTVINTVDPPLPDTVTELLTWIFERIGEVVYLPPHLMDACTSLCASGTAFFALMMEAA
                                                                                                                                                                                                                                                                                                       -----ADVQARHIVVSCAAGVTISSVEKKL----MAFQPAPKVIRCMTNTPVVVQ 125
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Search completed: January 31, 2002, 14:57:38 Job time: 203 sec

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Maximum Match 100%
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is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comr
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pir3:*
pir4:*
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E69682
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G69964
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S76767
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pyrroline-5-carbox
                                     probable pyrroline
Delta 1-pyrroline-
                                                      pyrroline-5-carbox
                                                                      pyrroline carboxyl
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
102	104	104	106	106.5	114.5	148.5	162.5	179	179.5	192.5	193.5	212.5	212.5	229	258.5
б. 5	6.6	6.6	6.8	6.8	7.3	9.5	10.4	11.4	11.5	12.3	12.3	13.6	13.6	14.6	16.5
349	451	272	348	1043	264	253	273	275	257	243	257	263	263	267	272
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A25952	S26441	F69855	A32512	н83329	F69100	н69219	F69602	C83816	E71850	G81310	F64664	E81243	H82015	G83760	D82321
glycerol-3-phospha	hypothetical prote	pyrroline-5-carbox	glycerol-3-phospha	probable RND efflu	conserved hypothet	pyrroline-5-carbox	pyrroline-5-carbox	non-essential gene	probable pyrroline	probable pyrroline	pyrroline-5-carbox	pyrroline-5-carbox	probable pyrroline	pyrroline-5-carbox	pyrroline-5-carbox

#### ALIGNMENTS

A;Gene: GDB:PYCR1; P5C; PYCR A;Cross-references: GDB:135716; OMIM:179035 A;Map position: 17pter-17qter C;Superfamily: pyrroline-5-carboxylate reductase C;Keywords: oxidoreductase; proline biosynthesis pyrroline-5-carboxylate reductase (EC 1.5.1.2) - human
N;Alternate names: P5C reductase
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999
C;Accession: A41770
R;Dougherty, K.M.; Brandriss, M.C.; Valle, D.
J. Biol. Chem. 267, 871-875, 1992
A;Title: Cloning human pyrroline-5-carboxylate reductase cDNA by complemental A;Reference number: A41770; MUID:92112821
A;Accession: A41770 밁 20 B δÃ 밁 9 밁 δõ В Qy В Query Match Best Local Similarity Matches 263; Conserv 181 117 1 1 MSVGFIGAGQLAYR----FTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETV TPSSPGKLLTRSLALGGK 312 ALHFLESGGFRSLLINAVEASCIRTRELQSMADQEKISPAALKKTLLDRVKLESPTVSTL SPSGHTKLLPRSLAPAGK MSVGFTGAGQLAFALAKGFTAAGVLAAHKIMASSPDMDLATVSALRKMGVKLTPHNKETV ALHVLESGGFRSLLINAVEASCIRTRELQSMADQEQVSPAAIKKTILDKVKLDSPAGTAL Conservative 83.3%; 82.7%; 27; Mismatches Score 1306; DB 1; Pred. No. 2.1e-96; ?7; Mismatches 22; Length 319; Indels 6 complementation Gaps 234 116 240 60 <u>ب</u> · 5

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submitted to the EMBL Data Library, Novem A; Reference number: 219796
A; Accession: T23765
A; Status: preliminary; translated from GB A; Molecule type: DNA A; Residues: 1-279 <MIL>
A; Residues: 1-279 <MIL>
A; Cross-references: EMBL: Z67995; PIDN: CAA A; Experimental source: clone M153
C; Genetics: A; Gene: CESP: M153.1
A; Map position: X
A; Introns: 23/1; 106/3; 177/3; 248/3
C; Superfamily: pyrroline-5-carboxylate re
                                                                                                                          A;Accession: JQ2334
A;Molecule type: DNA
A;Residues: 1-276 <VER>
A;Cross references: GB:M76538; NID:g166814; PIDN:AAA61346.1;
A;Cross references: GB:M76538; NID:g166814; PIDN:AAA61346.1;
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.;
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z5394
A;Accession: T51425
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                               pyrroline-5-carboxylate reductase (EC 1.5.1.2) [similarity] - Ar N;Alternate names: protein T913.100 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C;Accession: JQ2334; T51425 R;Verbruggen, N.; Villarroel, R.; Van Montagu, M. Plant Physiol. 103, 771-781, 1993 A;Title: Osmoregulation of a pyrroline-5-carboxylate reductase g. Reference number: JQ2334; MUID:94294559
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c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23765
R;Matthews, P.
  A;Cross-references: EMBL:AL391149
A;Experimental source: cultivar Cc
C;Comment; This enzyme is involved
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                                                                              A; Molecule type: DNA
A; Residues: 1-276 <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 ALHFLESGGFRSLLINAVEASCIRTRELQSMADQEKISPAALKKT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 MFAVIEGLADGGVKVGLPRDLALKLAAYTLLGAAKMVLETGIHPAQLKDDVQSPAGSSVY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKSDVVFLAVKPVHVSKVASEIAPALSKEHLVVSIALGITIRNIESLL---PTKSRVVRV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKIGFIGAGKMAQALARGLINSGRITADNIIASSPKRDEVFLDQCKALGLNTTHDNAEVV
This enzyme is involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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  proline biosynthetic pathway.
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pyrroline-5-carboxylate reductase (EC 1.5.1.2) - soybean
C;Species: Glycine max (soybean)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text.
C;Accession: S10186
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X16352; NID:g18723; PIDN:CAA34401.1; PID:g18724 A;Note: the authors translated the codon GAA for residue 115 as Pro and C;Superfamily: pyrroline-5-carboxylate reductase C;Keywords: oxidoreductase; proline biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: A soybean gene encoding Delta1-pyrroline-5-carboxylate reductase was A;Reference number: S10186; MUID:90340278 . A;Accession: S10186
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S10186
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C; Superfamily: pyrroline-5-carboxylate reductase
C; Keywords: oxidoreductase; proline biosynthesis
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A; Residues: 1-274 < DEL>
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A; Introns: 67/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Delauney, A.J.; Verma, D.P.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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187
                                      178
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                                                                                                                                                                                                                                    12 TLGFIGAGKMAESIARGAVRSGVLPPSR-IRTAVHFNLARRGAFESFGVTVLPSNDDVVR 70
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                    FMALD--ADGGYKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHA 235
                                                                                                                                                                                            HSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAIEALADGGVAAGLPRELALSLASQTVLGAATMVSKTGKHPGVLKDDVTSPGGTTIAGV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALD--ADGGYKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGFIGAGKMAESIARGVVASGVLPPNR-ICTAVHSNLNRRDVFESFGVNVFSTSEEVVKE
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                                                                                                               TNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYA 177
                                                                                                                                                       ESDVVVLSVKPQLVKDVVSKLTPLLTKHKLLVSVAAGTKL----KDLQEWAGNDRFIRVM 126
                                                                                                                                                                                                                                                                         SVGFIGAGQLAYRF----TAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETVK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HELEKGSFRATLMNAVVAAAKRSREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTPAAVGEAASVMSLGTGATEEDGAIVAMLFGAVGKILKADEKMFDAVTGLSGSGPAYIF 187
YLAIEALADGGVAAGLPRDLSLSLASQTVLGAASMVSQTGKHPGQLKDDVTSPGGTTITG
                                                                            PNTPAAVGQAASVMSLGGSATEEDGNIIAQLFGSIGKIWKAEEKYFDAITGLSGSGPAYV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDVVIFSVKPQVVKKAVTELKSKLSKNKILVSVAAGIKLNDLQE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84/1; 114/3; 139/1; 179/2; 214/3
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                             32.0%;
41.6%;
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                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                 Score 501.5; DB 1 Pred. No. 1.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 512.5; DB 1
Pred..No. 2.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                 11;
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236

LHFLESGGFRSLLINAVEASCIRTREL 262

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A; Molecule type: mRNÁ
A; Residues; 1-273 (WIL)
A; Cross-references: EMBL: X62842; N
A; Experimental source: Cv. Wando
C; Genetics:
A; Gene proC
C; Superfamily: pyrroline-5-carboxy
C; Keywords: oxidoreductase; proline
                                                                          A; Gene: proC; :
C; Superfamily:
                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-284 <SEE>
A;Cross-references: EMBL:AL049819; PIDN:CAB42663.1; GSPDB:GN00070; SCOEDB:SCE7.04c
                                                                                                                                                                                                                                                                                                                                 pyrroline-5-carboxylate reductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Date: 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable pyrroline-5-carboxylate reductase (EC 1.5.1.2) - garden pea C;Species: Pisum sativum (garden pea) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 C;Accession: T06477 R;Williamson, C.L.; Slocum, R.D. Plant Physiol. 100, 1464-1470, 1992 A;Title: Molecular cloning and evidence for osmoregulation of the d1-pyrroline-5-carboxy A;Reference number: 215706 A;Accession: T06477 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                        A; Reference number: 221603
A; Accession: T36286
                                                                                                                                                                                                                                                                             R; Seeger, K.J.; Harris, D.; submitted to the EMBL Data
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                                                                                                                                        A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                      C; Accession: T36286
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  Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
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                                                                                                                                                                                                                                                                                            K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGVHELEKGGFRGTLMNAVVAAAKRSREL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMPNTPAAVGQAASVMSLGGAATEEDANLISQLFGSIGKIWKADDKFFDAITGLSGSGPA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLGFIGAGKMAESIAKGASRSGVLPSSRIVTAHSNPSRR----AAFESIGITVLSSNDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAFMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRASNVVVFSVKPQLVKDVVLKLKPLLTKDKLLVSVAAGIKL----KDLQEWAGHERFIR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVGFIGAGQLAYRF----TAAGILSAHKIIA--SSPEMNLPTVSALRKMGVNLTRSNKET 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YIYLAIEALADGGVAAGLPRDLALSLASQTVLGAASMATLSGKHPGQLKDDVTSPGGTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKHSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108;
Similarity
                                                                                                   SCOEDB: SCE7.04c
                                                                            pyrroline-5-carboxylate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
  27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.6%; Score 479; DB 2;
40.1%; Pred. No. 9.3e-31;
tive 55; Mismatches 90
                                                                                                                                                                                                                                                                             Library, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID: g20850; PIDN: CAA44646.1;
  Score 423; DB 2;
Pred. No. 2.8e-26;
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                  Length
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                    284;
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C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: S76767 C;Accession: S76767 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watenabe, A.; Yemada, M.; Yas DNA Res. 3, 109-136, 1996 DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: pyrroline-5-carboxylate reductase C; Keywords: oxidoreductase; proline biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Synechocystis sp. (strain C; Species: Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:D90916; GB:AB001339; A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-267 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S74322; MUID:97061201 A; Accession: S76767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Variety: PCC 6803
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                    112 KVIRCMTNTPVVVQEGATVYATGTHALVEDGQL--LEQLMSSVGFCTEVEEDLIDAVTGL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250
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                                                 228 PGGATIHALHFLESGGFRSLLINAVEASCIRTREL 262
                                                                                                                                                               170 SGSGPAYAFMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCS
                                                                                                                                                                                                                   112 AIIRAMPNTPATV--GAGMTAIAANKMVEPDQLAKAKAIFSAVGNVVEVPENLMDAVTGV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 HALHFLESGGFRSLLINAVEASCIRTREL 262 :|: ||: ||: ||: ||: ||: ||: ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 YFFYLVEAMTDAGILLGLPRDKAHDLIVQSAIGAAKMLRDSGEHPVKLRENVTSPAGTTI
                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                           52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSVGFIGAGQLA----YRFTAAGILSAHKIIASSPEMNLPTVSALK-----KMGVNLTRS
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                                                                                                           SGSGPAYVALMIEALADGGVLAGLPRAIAQKLALQTVLGTAELIKETEEHPAQIKDKVTS
                                                                                                                                                                                                                                                                                                                                                                                     NKETVKHSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAP 111
PGGTTIAGVAVLEKMGFRSAIIEAVRAAYRRSQEL
                                                                                                                                                                                                                                                                                                                                 NQEAANVSEVLLLAVKPQVLDRVLASLAGGAN-RPLVISILAGVSLQRIQKGF----PDH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                            IQLGIIGGGVMAEAILARLIAEKTYAPEEIIVGEPH-----GARRDYLQKTYQVRVSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAIRELENHGVRAALIAALEAARDRSREL 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VMTNTPALVDEAMSVISAGTHATAAHLTHTEEIFGAVGKTLRVPESQQDACTALSGSGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFIGAGQLAYRFTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTR-----SNKET 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMTGAG-----WAPADLL-------VTARRERADELRARHGVTPVTNAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.9%; Score 421; DB 2; 38.5%; Pred. No. 3.7e-26; tive 47; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID:g1653715; PIDN:BAA18679.1; PID:g165 to the EMBL Data Library. June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 68
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A;Residues: 1-269 <DEU>
A;Cross-references: GB:J01665; NID:g147358; PIDN:AAA86433.1; PID:g147359
A;Cross-references: GB:J01665; NID:g147358; PIDN:AAA86433.1; PID:g147359
A;NOte: parts of this sequence, including the amino and carboxyl ends of the mature pi
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                       #;Deutch, A.H.; Smith, C.J.; Rushlow, K.E.; Kretschmer, P.J.
Nucleic Acids Res. 10, 7701-7714, 1982
A;Title: Esscherichia coli delta(1)-pyrroline-5-carboxylate reductase: gene sequence,
A;Reference number: A00385; MUID:83116986
A;Accession: A00385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Escherichia coli
C;Species: Escherichia coli
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 11-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome economic - - -
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C; Species: Escherichia coli
                                                                                                                                                A; Title: The complete genome sequence of Escherichia A; Reference number: A64720; MUID:97426617 A; Accession: B64767
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
A;Residues: 1-269 <BLAT>
A;Cross-references: GB:AE000145; GB:U00096; NID:g1786580; A;Experimental source: strain K-12, substrain MG1655
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                                                                                  A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHAL 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADIIFAAVKPGIMIKVLSEITSSLNKDSLVVSIAAGVTLDQLAR----ALGHDRKIIRAMP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGFIGCGNMG-KAILGGLIASGQVLPGQIWVYTPSPDKVAALHDKFGINAAESAQEVAQI
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35.9%;
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                                                                                                                                                                                                             coli K-12
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                                    PIDN:AAC73489.1; PID:g1786585;
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      Query Match
Best Local Similarity
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C;Superfamily: pyrroline-5-carboxylate reductase C;Keywords: oxidoreductase; proline biosynthesis F;2-273/Product: pyrroline 5-carboxylate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: part of this sequence, including the amino end of the mature protein, was con R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uV0418
pyrroline-5-carboxylate reductase (EC 1.5.1.2) precursor - Pseudomonas aeruginosa (st C;Species: Pseudomonas aeruginosa
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
JQ0418
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A;Map position:
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                     .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Comparison of proC and other housekeeping A;Reference number: JQ0418; MUID:90185238 A;Accession: JQ0418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                            A; Gene: proC; PA0393
                                                                                                                                                     A;Cross-references: GB:AE004476; GB:AE004091; NID:g9946234; PIDN:AAG03782.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                           A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337 A;Accession: H83597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 86, 107-111, 1990
                                                                                                                               C; Genetics:
                                                                                                                                                                                                                     A; Residues: 1-273 <STO>
                                                                                                                                                                                                                                                  A; Molecule type: DNA
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A; Residues: 1-273 <SAV>
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                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: JQ0418; H83597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 MALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 MFIEAMADAAVLGGMPRAQAYKFAAQAVMGSAKMVLETGEHPGALKDMVCSPGGTTIEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NTPALVNAGMTSVTPNALVTPEDTADVLNIFRCFGEAEVIAEPMIHPVVGVSGSSPAYVF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 NTPVVVQEGATYYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 ADIIFAAVKPGIMIKVLSEITSSLNKDSLVVSIAAGVTLDQLAR----ALGHDRKIIRAMP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 SDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 IGFIGCGNMG-KAILGGLIASGOVLPGQIWVYTPSPDKVAALHDQFGINAAESAQEVAQI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VGFTGAGQLAYRFTAAGILSAHKIIASSPEMNLPT---VSALR-KMGVNLTRSNKETVKH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.; Jeenes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFLESGGFRSLLINAVEASCIRTRELQSMADQEKIS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.J.; Kocher, H.P.; Haas, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.7%;
35.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TKCMEKSEKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 402.5; DB 1
Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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24.1%;

Score Pred.

377; DB 2; No. 1.2e-22;

#status experimental <MAT>

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N;Alternate names: profine blosynthesis protein proH
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: E69682: B32807
C;Accession: E69682
Bron, S; Brouillet, S; Bruschi, C, V; Caldwell, B; Capuano, V; Carter, N.M.; Chc
R;Kunst, F; Ogasawara, N.; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter
C; Bron, S; Brouillet, S; Bruschi, C, V; Caldwell, B; Capuano, V; Carter, N.M.; Chc
R;Kunsto, F; Ogasawara, N.; Moszer, I; Albert, H; Holsappel, S; Hosono, S; Hullo, M.F
N;Authors: Foulger, D; Fritz, C; Fujita, M.; Fujita, Y; Fuma, S; Galizzi, A,; Galler
Iech, J; Harwood, C.R.; Henaut, A.; Hilbert, H; Holsappel, S; Hosono, S; Hullo, M.F.
N;Authors: Lauber, J; Lazarevic, V; Lee, S,M.; Levine, A,; Liu, H; Masuda, S; Mueel
R; M.; Ogawa, K.; Ogiwara, A.; Oudega, B; Park, S.H.; Parro, V; Pohl, T.M.; Portetile
R; M; Holser, M.; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadaie, Y; Sato, T; Scanlon,
akeuchi, M.; Tamakoshi, A.; Tanaka, T; Terpstra, P; Tognoni, A; Tosato, V; Uchiyama,
A;Authors: Yoshikawa, H,F; Zumstein, E; Yoshikawa, H; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Stafine, nrollminary, nrollata and accession: E69682
A:Stafine, nrollminary, nrollata and accession.
                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: proH
C;Superfamily: pyrroline-5-carboxylate reductase
C;Keywords: oxidoreductase; proline biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-57,'A',59-69,'S',71-73,'T',75-92,'S',94-99,'T',101-126,'Q',128-158,'Q',160
A;Cross-references: GB:M24524; GB:M36988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Lowis, P.J.; Wake, R.G.

J. Bacteriol. 171, 1402-1408, 1989

A;Title: DNA and protein sequence conservation at the replication terminus in Bacillus A;Reference number: A32807; MUID:89155440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-270 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Bacillus subtilis
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                                                                                                                                                         Query Match
Best Local
                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13741.1; PID:g2634242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: B32807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 EAAIKSFQANGFEALVEQALNAASQRSAELAEQLGQ 273
                                    3 VGFIGAGQLAYRFTAAGILSAHKI----IASSPEMNLPTVSALR-KMGVNLTRSNKETVK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 IHALHFLESGGFRSLLINAVEASCIRTRELQSMADQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 AYFFLLMQAMTDAGEKLGLSRETASRLTLQTALGAAQMALSSEVEPAELRRRVTSPNGTT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NTPALLRQGASGLYA---NAQVSAAQCEQAGQLLSAVGIALWLDDEAQIDAVTAVSGSGP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 NTPVVVQEGAT-VYATGTHALVEDGQLLE--QLMSSVGFCTEVEEDL-IDAVTGLSGSGP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 ADVVVLSVKPQAMKAVCQALAPALKPEQLIVSIAAGIPCASLEAWL--GQPRP-VVRCMP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAFIGAGNMAASLIGGLRAQGVPAA-QIRASDPGAE-QRAKIAGEFAIDVVESNAEAVAD 63
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                                                                                                                                                   Similarity
                                                                                                                     Conservative
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                    22.0%; Score 345; DB 2; 34.6%; Pred. No. 4.1e-20;
                                                                                                    53; Mismatches 101; Indels
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<del>:</del>:
                                                                                                                                                                       Length 270;
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Pyrroline-5-carboxylate reductase homolog yqj0 - Bacillus subtilis
N;Contains: oxidoreductase (EC 1.-..)
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: G69964
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C:Superfamily: pyrroline-5-carboxylate reductase
C:Keywords: oxidoreductase
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N;Alternate names: B2168_C2_211 protein
C;Species: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U00018; NID:g467037; PIDN:AAA17233.1; PID:g467049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-294 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Description: Mycobacterium leprae cosmid B2168. A:Reference number: S72586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Smith, D.R.;
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                                                                                                                                                                                                                                                                                     288 QLR 290
                                                                                                                                                                                                                                                                                                                                                  261 ELQ 263
                                                                                                                                                                                                                                                                                                                                                                                                228 DRHSAEVAPLGAQVDVPAAQLRATITSPGGTTAAALRELERGGLRMVVDAAVQAAKIRSE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 EQH------PCQLKDNVCSPGGATIHALHFLESGGFRSLLINAVEASCIRTR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 ESQMDAVTAVSGSGPAYFFLLVEALVDAGVAVGLTRQVATELAAQTMAGSAAMLLERMDQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 KLPAGTP----VVRAMPNAAALVGAGVTVLAKGRFV----TGQQFEDVLAMFDAVGGVLTVP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 KLMAFQPAPKVIRCHTNTPVVVQEGATVYATGTHALVEDGQLLEQLMS----SVGFCTEVE 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 LVTSVTDAVENAMFVVVAVKPTDVESVMGDLVQAAAVANDSAEQVLVTVAAGVTITYLES 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 LTRSNKETVKHSDVLFLAVKPHIIPFILDEI-----GADVQARHIVVSCAAGVTISSVEK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 LQALKKSGGEKRFL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 LHFL-ESGGFRSLL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 PNTSSMIGASATAIALGKYVSEDLKKLAEALLGCMGEVYTIQENQMDIFTGIAGSGPAYF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 THTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 HSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 VAFIGAGSMA-EGMISGIVRANKIPKQNICVTNRSNTERLTELELQYGIKGALPNQLCIE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDLIDAVTGLSGSGPAYAFMALDA--DGGVKMGLPRRLAIQLGAQALLGAAKMLL---DS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DMDVLILAMKPKDAENALSSLKSRIQPHQLILSVLAGITTSFIEQSLLNEQP----VVRVM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robison, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.8%; Score 326.5; DB 2; Length 294; 36.2%; Pred. No. 1.4e-18; Indels 33
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A;Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A.; Lughidus, A.; Lardinols, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serora akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; A;Fitle: The complete genome seguence of the Gram-positive bacterium Bacillus subtilis. A;Accession: G69964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Hullo, M.F. Scetter, P.; Koningstein, G.; Krogh, S.; Kuether, F.; Koningstein, G.; Krogh, S.; Kuether, F.; Kuether, F.; Koningstein, G.; Krogh, S.; Kuether, F.; Kueth
                                                                                                                                                                                                                                                                                                                                                                                                                        pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Thermus aquaticus (strain HB27)
C;Species: Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 26-Aug-1999
C;Accession: JC2078
R;Hoshino, T.; Kosuge, T.; Hidaka, Y.; Tabata, K.; Nakahara, T.
Biochem. Biophys. Res. Commun. 199, 410-417, 1994
A;Title: Molecular cloning and sequence analysis of the proC gene encoding delta-1-pyrroA;Reference number: JC2078; MUID:94168609
A;Accession: JC2078
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A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: yqj0
C;Superfamily: pyrroline-5-carboxylate reductase
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-261 <HOS>
C; Superfamily: pyrroline-5-
C; Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                         Superfamily: pyrroline-5-carboxylate reductase
Matches
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                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDIIILAFKPKDAAESIDSIRPYIKDQ------LVISVLAGLTIETIQHYFGRKL-- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGFVGAGSMAEAMINGILQSGITKPEHIYITNRSNDERLIELKETYSVRPCRDKNEFFTH 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAIAGSGPAYVYRYIEAMEKAAQKVGLDKETAKALILQTMAGATDMLLQSGKQPEKLRKE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGLSGSGPAYAFMALDA--DGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDVLFLAVKP-----HIIPFILDEIGADVQARHIVVSCAAGVTISSVE----KKLMA 106
                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                    Conservative
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                                                                 20.6%; Score 323.5; DB 2; 33.9%; Pred. No. 2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Mismatches 113;
                              45;
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Pred. No. 1.8e-18;
                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                              107;
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                                   Indels
                                                                                                                        Length 261;
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: G83837
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A;Residues: 1-79 <STO>
A;Crossreferences: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05222.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A83650; MUID:20263314
A; Accession: G83837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyrroline-5-carboxylate reductase BH1503 [imported] - Bacillus halodurans (strain C-1
                                                                                                                                                                                                      D
                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                             Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: BH1503
C;Superfamily: pyrroline-5-carboxylate reductase
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                                              Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
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                                                236 LHFLESGGFRSLLINAVEASCIRTRELQSMADQE 269
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                                                                                                                                                                                                                                                    118 TNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYA 177
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                                                                                                    183 YYMVEAMERAAVQSGLTESEAKAFISQTLIGTGKRLEQTSKTAEELYKEVMSPGGTTEAG
                                                                                                                                                  178 FMALDA--DGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRLAFYGLGKMGRSILKGALERGFLRPEEYGYLGRTPERSR---ELAEPFGYRPLTRAD-
                                                                                                                                                                                                                                                                                                        66 QGTIIFLAMKPKNIEEAIEEIRGEITEKQLFTSVLAGTTTSYIETLLAHEVP----VVRTM 122
                                                                                                                                                                                                                                                                                                                                                         58 HSDVLFLAVKPHITPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             7 ITFLGAGSMA-ESIIAGLLSKKLLLPSQVIATNLCDEAKLTKLEDRYGICTTQNRQEAVR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VGFIGAGQLAYRFTAAGILSAHKIIASSP-EMNLPTVSALRKM----GVNLTRSNKETVK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LGMAERVLIAVQPRDFPALAPEI-----AHHRLGYISIMAGISTSVLARRL----DNR 105
LRVLEQQQMQQAIEEAITAAINRSRELGSTPSLE 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 323.5; DB 2;
Pred. No. 2.2e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Search completed: January 31, 2002, 14:54:14
Job time: 44 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                   SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_invertebi
                                                                                                                                                                                                                                                                                                                                                                                                           473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-912-717-1
1567
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                   sp_organelle:*
sp_phage:*
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sp_bacteria:*
sp_fung1:*
                                                                                                                  sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                              473505
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 3 3 4 4 4 5 5 6 6 7 7 7 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
1231.5 898 537.5 522.5 522.5 503 500.5 469 469 448 448 4423 399 380 399 380 376 376 323.5	Score
578.5 578.6 36.9 36.9 33.3 33.3 30.7 30.7 20.7 20.7 20.8 20.8	Query Match Length DB
319 279 279 274 274 274 273 273 270 280 280 280 280 270 272 272 272 273 279 279	ength [
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09Y5J4 0918Q4 02118Q4 02118Q4 09H896 09EJ3 09AYM3 09AYM3 09AYM3 09AYM3 09H199 09K3G1 09X3G1 09X3G1 09K3G8	ID
09y5j4 homo sapien 09hbg4 homo sapien 021544 caenorhabdi 09h896 homo sapien 09dcc4 mus musculu 09vej3 drosophila 09aym3 vigna ungui 09ayf8 drosophila 09of64 drosophila 09h99 methanosarc 087725 clostridium 09x8g1 streptomyce 09k308 bacillus ce 09d0x2 mus musculu 09ng4 leishmania 09h16 thermoplasm 09ra98 nostoc sp. 09kcr6 bacillus ha 027722 plasmodium	Description

4.4 4.5	440 410 421		28 30 31 32	20 21 22 23 24 25 27
			263.5 258.5 258.5 252.5	
0.00 0.50 0.4	9.7 9.6 7.3 6.8	14.6 13.6 13.6 12.3	16.5 16.5 16.5	20.4 19.2 19.0 18.9 18.7 18.7
1043 350 8817				255 262 262 262 262 275
2 Q910V6 13 Q98SJ9 2 Q53840		2 Q9KEG5 2 Q9K1N1 2 Q9JWW2 2 Q9PNL8 2 Q9FNL8		2 Q9WZ47 2 Q9EZ83 2 Q9PAO8 2 Q9CEF7 1 Q9YFV4 3 Q9P7Y7 3 Q9P7Y7 3 Q9P7Y7
Q910v6 p Q98sj9 Q53840 p	7		Q9ru71 Q9fdk7 Q9aau9 Q9aug5 Q9kuq5 Q9als9 Q9als9	
910v6 pseudomonas 910v6 pseudomonas 998sj9 salmo salar 93840 polyangium	arabidopsis bacillus su methanobact methanobact	bacillus ha neisseria m neisseria m campylobact	deinococcus zymomonas m caulobacter vibrio chol streptococc	thermotoga bradyrhizob xylella fas lactococcus aeropyrum p schizosacch pasteurella
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## ALIGNMENTS

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RESULT
Q21544
ID Q21544
ID Q2
AC Q2

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HOROTHETICAL 28.5 KDA PROTEIN.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu J., Han L.H.;
"Novel Human cDNA clones with function of inhibiting cancer cell growth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P., Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9НВQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9нвQ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000304; P5CR.
pfam; PF01089; P5CR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF218000; AAG17242.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
                                                                                                                                                                                                                       Q21544
Q21544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 272 AA; 28471 MW; 0BC71EA751F7F8F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298
                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                          Caenorhabditis elegans.
                                                                                                                 M153-1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                          181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYAFMALD--ADGGYKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGAT
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                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSVGFIGAGQLAYR----FTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSVGFIGAGQLAFALAKGFTAAGVLAAHKIMASSPDMDLATVSALRKMGVKLTPHNKETV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QHSDVLFLAVKPHIIPFILDEIGADIEDRHIVVSCAAGVTISSIEKKLSAFRPAPRVIRC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHSDVLFLAVKPHIIDFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRC 116
                                                                                                                                                                                                                                                                                                                                                                                          AFTALDALADGGVKMGLPRRLAVRLGAQALLGACQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                     AFMALD--ADGGVKMGLPRRLAIQLGAQALLGAAK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180;
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                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.3%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches
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                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 898; DB 4
Pred. No. 1e-63;
                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                             279
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                                                                                                                                                                                                                                                                AA.
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                                        Rhabditida; Rhabditoidea;
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RESULT
Q9H896
ID 999
DT 01
DT 01
DT 02
DT 
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Best Local (
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Bonfield J., Burton J., Connell M., Copsey T., Copler J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston R.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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EMBL; Z67995; CAA91943.1; -.
InterPro; IPR000304; P5CR.
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                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ13852 FIS, CLONE THYRO1000934, WEAKLY SIMILAR TO PYRROLINE-5-
CARBOXYLATE REDUCTASE (EC 1.5.1.2).
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   TISSUE-THYROID GLAND; Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Isogai T., Ota T., Hayashi K., Sugano S., Takahashi Fujii A., Hara H., Nishikawa T., Nagai K., Sugano S., Komai F., Hara R., Takeuchi K., Tanase T., Nomura Y., Tojiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 MFAVIEGLADGGVKVGLPRDLALKLAAYTLLGAAKMVLETGIHPAQLKDDVQSPAGSSVY
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                Yamamoto J.,
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashariaki V.
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Submitted (AUG-2000) to the EMBL
EMBL; AK023914; BAB14721.1; -.
InterPro; IPR000304; P5CR.
Pfam; PF01089; P5CR; 1.
PROSITE; P500521; P5CR; 1.
SEQUENCE 274 AA; 28663 MW; E
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Q9DCC4;
01-JUN-2001
                          "Functional annotation of a full-length mouse cDNA Nature 409:685-690(2001).
EMBL: AK002912; BAB22451.1; -
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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                                                                                                                           Hayashizaki Y.;
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EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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              RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A. Galle R.F.,
RA Adams M.D. (Celniker S.E., Li P.W., Hoskin: ..., Galle R.F.,
RA Adams M.D. (Celniker S.E., Richards S., Ashburner ..., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner ..., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner ..., Henderson S.N.,
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RA George R.A., Lewis S.E., Richards M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards M.D., Ralson C.R., Miklos G.L.G.,
RA George R.A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barlow R.M., Bayter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrill J.F., Aqbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beesson K.Y., Benos P.Y., Berman B.P., Bayraktaroglu L., Beasley E.M.,
RA Beesson K.Y., Benos P.Y., Berman B.P., Brockstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davles P.,
RA Dudson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Barvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ilbeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krantson J.A., Ketchum K.A.,
RA Mchult S.M., Moy M., Murphy B., Murphy L., Muzyy D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyy D.M., Nelson D.L.,
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01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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       Murphy B.,
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       Murphy L.,
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A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syirskas R., Tector C., Tunner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).

BELLBASC, EBENDORSEIS. - CESAO.
                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TremBLrel. 17, 01-JUN-2001 (TremBLrel. 17, 01-JUN-2001 (TremBLrel. 17,
                                                                                                    SEQUENCE
                                                                                                                      EMBL;
                                                                                                                                     Submitted
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Vigna unguiculata (Cowpea).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids I; Fabales; Fabaceae; Papilionoideae; Vigna.
                                                                                                                                                                                                                                                                                                                            VUP5CR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                           Q9AYM3;
                                                                                                                                                                                                                                                                                                                                                                                                                 Q9AYM3
                                                                                                                 "Drought inducible gene from cowpea.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AB056453; BAB33038.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMIEALADGAVHMGMPRDLAYRLASQTVLGAGHMVRDSGMHPGQLKDGVTSPAGSTAAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDVVFVSVKPQVVPSVLSEI-QPLSSGKLFLSVAMGITLSTIESSL---SPQARVIRVMP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt IGFLGGGNMAKALAKGFLAAGLAKPNTLIASVHPADKLSLQSFQSLGVETVIKNAPVVQQ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pro; IPR000304; P5CR. PF01089; P5CR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01089; P5CR; 1.
PS00521; P5CR; 1.
273 AA; 28099 MW;
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                  28496 MW;
                              31.9%;
41.5%;
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              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation updat
            Score 500.5; DB 1
Pred. No. 4.5e-32;
51; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 503; Ub U,
No. 2.8e-32;
                                                                                                  BC10C7F8F84D7570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563754C62ACE77AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             274 AA
                                              DB 10;
                                                                                                                                                                                                                                                                                                                                           update)
              90;
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                                                                                                                                                                                                                                      core eudicots; Rosidae;
; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 273;
                                              Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
              17;
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            Gaps
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RESULT
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mcrkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mcunt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong A.H., Wang X.,
Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Baxendale J., Bayaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Diletz S.M.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Borkova D., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris M. J., Harmander J. Hernander J. Hernand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLGFIGAGKMAESIARGAVRSGVLPPSRIRTAVHSNPARR----TAFESFGVTVLSSNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVGFIGAGQLAYRF----TAAGILSAHKI---IASSPEMNLPTVSALRKMGVNLTRSNKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVKHSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVI 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13,
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Best Local
"Cioning and sequence analysis of the gene encoding pyrroline carboxylate reductase from Drosophila melanogaster.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR098020; AAC70780.1; -
ENJBASE; FBGN0015781; P5cr.
InterPro; IPR000304; P5CR.
Pfam; PF01089; P5CR; 1.
PROSITE; PS00521; P5CR; 1.
PROSITE; P500521; P5CR; 1.
                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PYRROLINE 5-CARBOXYLATE REDUCTASE.
                                                                                                                                                     Misener S.R., Walker V.K.;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                              P5CR OR CG6009
                                                                                                                                                                                                                                                                                                                                                                                               096643
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EMBL; AE003724; AAF55626.1; -.
EMBL; AF170829; AAD49740.1; -.
ElyBase: FB900015781; P5Cr.
InterPro; IPR000304; P5Cr.
InterPro; IPR000304; P5CR.
Pfam; PF01089; P5CR; 1.
PROSITE; PS00521; P5CR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 VAGCGPAFVYTIIEALADGGVKQGVPRQMALQFAAQTLLGAAKTVLLTGKHPAVLRDEVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 SPGGATIHALHFLESGGFRSLLINAVEASCIRTREL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 LSGSGPAYAFMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 SELKVIRTMPNTSMQVGEGCTVYTGNARVSHHDLEKIHLMLNALGLAQQVPESMIDAVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "High density of unrelated genes showing overlapping and intraintronic transcription units in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misener S.R., Walker V.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VGEIGAGQLAYR----FTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETVKH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPGGATIVGVHELEKGNLRSTLINAVEKSSQRSAEL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP-KVIRCMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDIVFICVKPH----MLTPCAAQLKYKHVPSAKDASKLVVSVLAGTSLETLEEAFSFMGS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDVLFLAVKPHIIPFILDEIGADVQARHI------VVSCAAGVTISSVEKKLMAFQP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGFIGGGNMAYAIGSGLVRCGIVKASQVQVSGP--HIENLQRWRDLGAVTCDDNCMVLEH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., .A., Myers E.W., Rubin G.M., Venter J.C.; nome sequence of Drosophila melanogaster."; 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 AA; 29621 MW; D3D4FD9611574684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.7%; Score 481; DB 5; 39.1%; Pred. No. 1.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                       280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 280;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang J.K., White A.K., Kuettner H.C., Boccazzi P., Metcalf W.W.; "Molecular and genetic analysis of proline biosynthesis in the methanogenic archaeon Methanosarcina acetivorans C2A.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF305580; AAG22033.1;
181 FPVIEAMADGAVLEGMDRKSALTLAAQTVLGAAKMALETGMHPGELKDMVTSPAGTTIQG
                               178 FMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHA 235
                                                                 121 PNIAATVSEAASGIAPGKNATPEDLKAALEIFSAVGTAVQVPESLMDAVTGLSGSGPAFI 180
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C2A;
                                                                                                 118 TNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanosarcina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29нн99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09нн99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001
                                                                                                                                     64 ESDILILAVKPQTLSSVLSNLKNEITSEKLVISIAAGVPLSTYEDALL---EGTRVVRVM 120
                                                                                                                                                                    58 HSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 SPGGATIVGVHELEKGNLRSTLINAVEKSSQRSAEL 277
                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 SPGGATIHALHFLESGGFRSLLINAVEASCIRTREL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 VAGCGPAFVYTIIEALADGGVKQGVPRQMALQFAAQTLLGAAKTVLLTGKHPAVLRDEVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 LSGSGPAYAFMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AP-KVIRCMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTG
                                                                                                                                                                                                       6 IGFIGAGKMGSALMQGTIKAGIVTPENIGAS--DVYEPFLKDLQAKLGIRVSTDNAVIVR 63
                                                                                                                                                                                                                                        3 VGFIGAGQLAYRF----TAAGILSAHKIIASSPEMNLPTVSALR-KMGVNLTRSNKETVK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 SDVLFLAVKPHIIPFILDEIGADVQARHI-----VVSCAAGVTISSVEKKLMAFQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 38.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VGFIGAGQLAYR----FTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETVKH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 IGFIGGGNMVYAIGSGLVRCGIVKASQVQVSGP--HIENLQRWRDLGAVTCDDNCMVLEH 65
                                                                                                                                                                                                                                                                                                                                                                   Pro; IPR000304; P5CR.
PF01089; P5CR; 1.
TE; PS00521; P5CR; 1.
NCE 270 AA; 27943 MW;
                                                                                                                                                                                                                                                                                        106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELKVIRTMENTSMQVGEGCTVYTGNARVSHHDLEKIHLMLNALGLAQQVPESMIDAVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDIVFICVKPH----MLTPCAAQLKYKHVPSAKDASKLVVSVLAGTSLQTLEEAFSFMGS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106;
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                           29.1%; Score 456; DB 1; Length 270; 39.7%; Pred. No. 1.5e-28;
                                                                                                                                                                                                                                                                             52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 469; DB 5; Length 280;
Pred. No. 1.5e-29;
1); Mismatches 97; Indels 22;
                                                                                                                                                                                                                                                                                                                                                               50EC656AFC10B1CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 AA
                                                                                                                                                                                                                                                                           97; Indels
                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                         Gaps
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087725
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Q9X601
ID Q9X801
ID Q9X801
AC Q9X801
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DT Q1-NOV
DT Q1-NOV
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DE PYRROL
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OS Strept
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087725;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NUV-1998 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene proC.",
gene proC.",
gubmitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ010739; CAA09332.1;
InterPro; IPR000304; P5CR.
pfam; PF01089; P5CR; 1.
pROSITE; PS00521; P5CR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium sticklandii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pyrroline-5-carboxylate reductase and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kenklies J., Ziehn R., Fritsche K., Andreesen J.R., Pich A.; "Proline biosynthesis in Clostridium sticklandii: Purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-HF, DSM 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 LHFLESGGFRSLLINAVEASCIRTREL 262
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                                                                                                                                               Q9X8G1;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2001 (TrEMBLrel. 17,
PYRROLINE-5-CARBOXYLATE REDU
                                                        Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                      SCE7+04C
                                                                                                                                                                                                                                                                                                    Q9X8G1
   NCBI_TaxID=1902;
                                  Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 IHALHFLESGGFRSLLINAVEASCIRTREL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTMPNTPSMVSEGMTAICPNSNIASEELELLVKLIESFGAVEIIEEKLFDAVVAVSGSSP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAEKCDIVFLAVKQNLYEMVMKEIKDSVTKDKIFVSIAPGKTMEFLEAHLGAY---AKIL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVKHSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGFIGCGNWAQAMISALVKSKLIESNQIIVSNRSKNI-----LEKMNKEYGITIAANNIE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGFIGAGQLAYRFTAA----GILSAHKIIASSPEMNLPTVSALRKM----GVNLTRSNKE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RCMTNTPVVVQEGATVYATGTHALVEDGOLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYVFMFIEAMADAAVIQGMPRAQAYRFAAQAVLGSAKMVLESKSHPGELKDMVCSPGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYAFMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEAVAVLEERGMRSAVIEAMRKCAOKSKEM 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 AA; 28902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 51; Mismatches
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.6%;
                                                                                                                                                     12, Last sequence update)
17, Last annotation update)
REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score 448; DB 2;
pred. No. 6.5e-28;
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                                                                                                                                                                                                                                                                                                                 284
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Q9K308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seeger K.J., Harris D.;
"A set of ordered cosmids and a detailed genetic and physical map
"A set by Streptomyces coelicolor A3(2) chromosome.";
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996). EMBL; AL049819; CAB42663-1; ...
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Interpro; IPR000304; P5CR; 1.
Pfam; PF01089; P5CR; 1.
PROSITE; PS00521; P5CR; 1.
SEQUENCE 284 AA; 29806 MW;
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                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
                                                                                                                                                                                                                                                             Q9K308;
           Okstad O.A., Agasse H., Lereclus D., Kolsto A.B.;
"20 kb DNA sequence surrounding the hblA hemolytic enterotoxin locus from Bacillus cereus ATCC 14579.";
                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                               Bacillus cereus.
                                                                                                                                                                                                                                                                              Q9K308
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                             STRAIN=ATCC 14579;
                                                                                                                                                                                                                                                                                                                                                                                       234 HALHFLESGGFRSLLINAVEASCIRTREL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 YAFMALDA--DGGVKMGLPRRLATQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 VMTNTPALVDEAMSVISAGTHATAAHLTHTEEIFGAVGKTLRVPESQQDACTALSGSGPA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 CMTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPA 175
                                                                                SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=1396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 VKHSDVLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GFIGAGQLAYRFTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTR------SNKET 55
                                                                                                                                                                                                                                                                                                                                                                                                                       YFFYLVEAMTDAGILLGLPRDKAHDLIVQSAIGAAKMLRDSGEHPVKLRENVTSPAGTTI 249
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                                                                                                                                                                                                                                                                              PRELIMINARY;
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40.1%; Pred. No. 7e-26;
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e EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                     272 AA
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A Kawal J. Shingawa A. Shibata K. Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Basole G., Ouackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nanon H., Baldarelli R., Barsh G.,
A Sahai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Barownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A RA Lyons P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
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EMBL; AJ007795; CAB96939.1; ...
EMBL; AJ237785; CAB69790.1; ...
InterPro; IPR000304; P5CR.

Pfam; PF01089; P5CR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 LHFLESGGFRSLLINAVEASCIRTRELQSMADQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 YMFIEAMADAAVLGGMPRKQAYKFAAQAVLGSAKMVLETGIHPGELKDMVCSPSGTTIEA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 PNTPALVGEGMSALCFNEMVTEKDIKEVLNIFNIFGQTEVINEKLMDVVTSISGSSDAYV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B. "Sequence analysis of three Bacillus cereus loci under PICR-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 FMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 TNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAYA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20055637; PubMed=10589720;
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SEQUENCE 254 AA;
126 EGATVYATGTHALVEDGOLLEGLMSSVGFCTEVEEDLIDAVTGLSGSGPAYAFMALDA--
                                                                                                                                                                                                                                                                                                                                                        Selenke L.M., Porter-Kelley J.M., Chaudhuri G.; "Cloning and characterization of Leishmania P5CR gene."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF241824; AAF64050.1;
                                                                                                                                                                                                                                                                                                                PROSITE;
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01-OCT-2000 (TrEMBLrel. 15, Last seq.
01-JUN-2001 (TrEMBLrel. 17, Last annu
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"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK004291; BAB23352.1;
MCD: MCI:1913444; 1110058B13Rik.
InterPro; IPR000304; P5CR.
                                                53 VKPNGIVPVLETIKEKITPSKLVISMAAGVPMATIENHC---PPKTKVVRVMPNIPSFVG 109
                                                                                66 VKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMTNTPVVVQ 125
                                                                                                                                              18 AGILSA-----HKII----ASSPE--MNLPTVSALRKMGVNLTRSNKETVKHSDVLFLA 65
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Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                2 AGMLKAKVLGPEHTFICNRRASTNERLVSLYHVSSVGAV-----ELAEKSDIIILG 52
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

AAB20584 RESULT Hillman JL, Baughn MR, Corley NC; WPI; 2000-548292/50. 18-JUN-1998; nootropic; neuroprotective; osteopathic; cytostatic; antiParkinsonian; cardiant; osteopathic; ophthalmological; hepatotropic; gene therapy; neuronal disorder; connective tissue disorder; cell proliferation; akathesia; Alzheimer's disease; amnesia; dementia; Parkinson's disease; cystic fibrosis; myocardial fibrosis; osteoporosis; Marfan syndrome; (INCY-) INCYTE PHARM INC 18-JUN-1998; 08-AUG-2000. US6100075-A. Synthetic. cirrhosis, leukaemīa, lymphoma, sarcoma, bone marrow cancer Human; delta 1-pyrroline-5-carboxylate reductase homologue; p5CRH; Human delta 1-pyrroline-5-carboxylate reductase homologue protein. 13-DEC-2000 (first entry) AAB20584 standard; Protein; 314 AA AAB20584; μ 98US-0099676 98US-0099676.

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disgrosing, treating or preventing neuronal disorders, connective tissue disorders, or disorders of cell proliferation. These may be applied to CC any subject, e.g. dogs, cats, cows, horses, rabbits, monkeys, or CC any subject, e.g. dogs, cats, cows, horses, rabbits, monkeys, or CC and quantitate gene expression in biopsied tissues where expression of the polypeptide may correlate with the disease. The diagnostic assay may CC be used to determine absence, presence, and excess expression of the CC polypeptide, and to monitor regulation of the polypeptide levels during CC therapeutic intervention. The polypeptide or its fragments are useful CC for treating or preventing neuronal disorder (e.g. akathesia, CC connective tissue disorder (e.g. cystic fibrosis, myocardial fibrosis, custhosis, leukaemia, lymphoma, sarcoma or bone marrow cancer). CC (e.g. cirrhosis, leukaemia, lymphoma, sarcoma or bone marrow cancer). CC libraries of compounds in any of several drug-screening techniques.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reductase homologue (p5CRH). p5CRH has nootropic, neuroprotective, osteopathic, cytostatic, antiparkinsonian, cardiant, osteopathic, cytostatic, antiparkinsonian, cardiant, osteopathic ophthalmological and hepatotropic activities, and can be used in contractive and contractive therapy. p5CRH and the polynucleotides encoding it are useful for therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents human delta 1-pyrroline-5-carboxylate reductase homologue (P5CRH). p5CRH has nootropic, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1A-E; 32pp; English.
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Human; pyrroline 5'-carboxylate reductase; Py-CR; P5CR
                                                                              06-JUN-2001
                                                                                                                                                    AAB74779 standard; Protein;
                                        Human Py-CR protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                             301 KLLTRSLALGGKKD 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVGFIGAGQLAYRFTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETVKHSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 msvgfigagqlayrftaagilsahkiiasspemnlptvsalrkmgvnltrsnketvkhsd 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        vlflavkphiipfildeigadvqarhivvscaagvtissvekklmafqpapkvircmtnt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLFLAVKPHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMTNT 120
                                                                                                                                                                                                                                                                                                              LDADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHALHFLE
                                                                                                                                                                                                                                                                                                                                                                                     klitrslalggkkd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 AA;
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                                                                              (first entry)
                                                                                                                                                                                                                                                314
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 Mismatches

                                                                                                                                                         320 AA
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ID AAB7
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Matches 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a human protein designated Py-CR, which is homologous to the human pyrroline-5'-carboxylate reductase (P5CR) (EC1.5 1.2). The present invention also describes methods for the application and production process of the Py-CR polynucleotide and protein sequences. The present sequence represents the human Py-CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu L, Fu Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human protein and its code sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF81847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYFU-) UNIV FUDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein as given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 16; 20pp; Chinese.
        Human; pyrroline 5'-carboxylate reductase; Py-CR; P5CR
                                  Human P5CR protein
                                                           06-JUN-2001 (first entry)
                                                                                  AAB74780;
                                                                                                         AAB74780 standard;
                                                                                                                                                                                                                                                                                                              295 TPSSPGKLLTRSLALGGKKD 314
                                                                                                                                                                                                                                                               181 afmaldaladggvkmglprrlaiqlgaqallgaakmlldseqhpcqlkdnvcspggatih
                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                      117 MINTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAY 176
                                                                                                                                                                    301
                                                                                                                                                                                                                  241
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVGFTGAGQLAYR----FTAAGILSAHKITASSPENNLPTVSALRKMGVNLTRSNKETV 56
                                                                                                                                                                                                                                                                                                                                                                                                           1\ {\tt msvgfigagglanalargftaagilsahkilasspemnlptvsalrkmgvnltrsnketv}\ 60
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                                                                                                                                                                                                                                                                                                                                                                         KHSDVLFLAVKDHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRC 116
                                                                                                                                                                                                                                                                                                                                                              khsdvlflavkhliipfildeigadvqarhivvscaagvtlssvekklmafqpapkvirc 120
                                                                                                                                                                                                                 tpsspgklltrslalggkkd
                                                                                                                                                                                                                                        ALHFLESGGFRSLLINAVEASCIRTRELQSMADQEKISPAALKKTLLDRVKLESPTVSTL 294
                                                                                                                                                                                                                                                                                      AFMALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99CN-0107071
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                                                                                                             Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1509; DB 22;
Pred. No. 3.3e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preparation and application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 320;
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Best Local
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         Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                       Human protein sequence SEQ ID NO:11795.
                                                                                                 AAB93027
                                                                                                                   AAB93027 standard; Protein; 212 AA
                                                                    26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a human protein designated Py-CR, which is homologous to the human pyrroline-5'-carboxylate reductase (P5CR) (EC1.5 1.2). The present invention also describes methods for the application and production process of the Py-CR polynucleotide and protein sequences. The present sequence represents the human P5CR protein which is used in comparison with the human Py-CR protein in
                                                                                                                                                                                301 spsghtkllprslapagk 318
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                          295 TPSSPGKLLTRSLALGGK 312
                                                                                                                                                                                                                            241 alhvlesggfrsllinaveascirtrelgsmadgegvspaaikktildkvkldspagtal
                                                                                                                                                                                                                                        235 ALHFLESGGFRSLLINAVEASCIRTRELOSMADOEKISÞAALKKTLLDRVKLESPTVSTL 294
                                                                                                                                                                                                                                                                                                                                                      117 MTNTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLIDAVTGLSGSGPAY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human protein and its code sequence, preparation and application
                                                                                                                                                                                                                                                                                                                              121 mtntpvvvregatvyatgthaqvedgrlmeqllstvgfcteveedlidavtglsgsgpay 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an example from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-211749/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYFU-) UNIV FUDAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVGFIGAGOLAYR----FTAAGILSAHKIIASSPEMNLPTVSALRKMGVNLTRSNKETV 56
                                                                                                                                                                                                                                                                                                                                                                                qhsdvlflavkphiipfildeigadiedrhivvscaagvtissiekklsafrpaprvirc 120
                                                                                                                                                                                                                                                                                                                                                                                               KHSDVLFLAVKPHIIPEILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRC 116
                                                                                                                                                                                                                                                                                                                                           ពេយព័ពល័ពីពិពេលវិបនចំពន់ចំពេច បើពេយពេចពេយ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99CN-0107071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%; Score 1306; DB 22; 82.7%; Pred. No. 1.9e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 319;
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283 RVKLESPTVSTLTPSSPGKLLTRSLALGGKKD 314

rvklesptvstltpsspgklltrslalggkkd 212

223 DNVCSPGGATHALHFLESGGFRSLLINAVEASGIRTRELQSMADQEKISPAALKKTLLD 282

dnvcspggatlhalhflesggfrsllinaveascirtrelgsmadqekispaalkktlld

180

61 avtglsgsgpayafmaldaladggvkmglprrlaiglgagallgaakmlldseghpcqlk 120

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                                                                                                                                 Query Match
Best Local
                                                                                                               Matches 210;
                                                                                                                                                                                                                             sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'end sequence/3'end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by cDNAs easily without any specialised methods. AAH03166 to AAH13638 and AAB35893 represent human amino acid sequences; and AAH13629 to AAH13632 of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end
                                                                                                                                                                                                  Sequence
165 AVTGLSGSGPAYAFWALD--ADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEOHPCQLK 222
                                                105 MAFQPAPKVIRCMTWTPVVVQEGATVYATGTHALVEDGQLLEQLMSSVGFCTEVEEDLID 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 11795; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-318749/34.
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02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999;
27-AUG-1999;
                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-2000;
                                1\ \verb|mafqpapkvircmtntpvvvqegatvyatgthalvedgqlleqlmssvgfcteveedlid|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000EP-0116126.
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                                                                                                                                                                                                  212 AA;
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                                                                                                               Conservative
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2000JP-0183767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T, Wakamatsu A, Nagai K,
                                                                                                                            66.7%;
                                                                                                          0; Mismatches
                                                                                                                     Score 1045; DB 22; Length 212; Pred. No. le-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate cancer antigen protein sequence SEQ ID NO:1218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB56640 standard; Protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US05988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                      cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antlinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer \dot{}
                                                                                                                                                                                                                                                                                                    gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAP16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1636-1637; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF15843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                       or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                         Sequence
                              σ
187 VKMGLPRRLATQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATTHALHFLESGGFRS 246
                                                                                                                                  69 HIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMTNTPVVVQEGA 128
                                                                                                                                                                                      Local Similarity
                                                                                                 9 hiipfildeigadiedrhivvscaagvtissiekklsafrpaprvircmtntpvvvrega 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-587513/55.
                                                                                                                                                                         208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM
                                                                                                                                                                                                                                                           255 AA;
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0124270
                                                                                                                                                                           66.5%; Score 1042; DB 21; Length 255; 84.6%; Pred. No. 2.8e-103; ltive 19; Mismatches 17; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OXRE-14; oxidoreductase; pyrroline-5-carboxylate-reductase; antiproliferative; anticancer; hepatotropic; antiviral; antiasthmatic; nootropic; neuroprotectant; antiparkinsonian's; antisclerotic; anxiolytic; antischizophrenic; anti-inflammatory; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human OXRE-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY92517 standard; Protein; 274 AA.
                                                                                                                                    06-OCT-1998;
02-DEC-1998;
10-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 llinaveascirtrelqsmadqeqvspaaikktildkvkldspagtalspsghtkllprs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 LLINAVEASCIRTRELQSMADQEKISPAALKKTLLDRVKLESPTVSTLTPSSPGKLLTRS
                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                 06-OCT-1999;
                                                                                                                                                                                                                                                              Modified-site
                                                                                                              (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                             WO200020604-A2
with decreased expression or activity of oxidoreductase molecules
        purified polypeptide for treating or preventing disorders associated
                                N-PSDB; AAA09388.
                                               WPI; 2000-303785/26
                                                                  Yang J;
                                                                               Hillman JL,
                                                                                          Lal P,
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                                                                                         Guegler KJ,
                                                                                Bandman O,
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                                                                                                                                       98US-0155202.
99US-0123911.
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                                                                                                                                                                                                                                                                                    /note=
259
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109
                                                                                                                                                                                                                                                                                                                                                     /note= "potential phosphorylation site"
108
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "for delta 1-pyrroline-5-carboxylate reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                  /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= signature_sequence
                                                                                                                                                                                                                                                                         /note=
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                                                                                  Gorgone GA, Cc
O, Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                           "potential phosphorylation site"
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                                                                                  Corley NC, Ban
Y, Au-Young J,
                                                                                              Baughn MR,
                                                                                     Yue H,
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Claim 1; Page 84; 97pp; English

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AAB95591
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C The polypeptides are useful for treating or preventing a disorder associated with decreased expression or activity of OXRE. Antagonists of CC associated with decreased expression or activity of OXRE. The disorder associated with CC increased expression or activity of OXRE. The disorders include cell CC increased expression or activity of OXRE. The disorders (leukemia, CC increased expression or activity of OXRE. The disorders (leukemia, CC increased expression and hyperpituitarism, hypothyroidism and CC increased expression and hyperpituitarism and hyperpituitarism and hyperpituitarism and hyperpituitarism and hyperpituitarism and hyperpituitarism and hypothyroidism and cc. Activity and hypothyroidism and cc. Activity and hypothyroidism and hyperpituitarism and hyperpituitarism, hypothyroidism and cc. Activity and hypothyroidism and
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Best Local
             (HELI-) HELIX RES INST
                                                                                             11-JAN-2000;
02-MAY-2000;
                                                                    09-JUN-2000;
                                                                                                                                               27-AUG-1999;
                                                                                                                                                                     29-JUL-1999;
                                                                                                                                                                                                                                                                                                                               EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                    28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                                                 HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:18269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB95591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 -AFMALDADGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQHPCQLKDNVCSPGGATIHA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Local Similarity 45.38;
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                                                                                          99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                  2000JP-0241899
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CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence 1s selected from those defined in CC in gene therapy. The primer sets can be used in antisense therapy and CC particularly full-length cDNAs. The primers are useful for synthesising polynucleotides, CC detection and/or diagnosis of the abnormality of the proteins encoded by CC clul-length cDNAs. The primers allow obtaining of the full-length CC clul-sets of the full-length cDNAs. The primers allow obtaining of the full-length CC clul-sets of the second methods. AAH03166 to AAH13628 and CC clul-sets of the comprise allow obtaining of the full-length CC clul-sets of the comprise and comprise and comprise compresent human cDNA sequences; AAB92446 to CC clubs seasily without any specialised methods. ABH03166 to AAH13628 and CC clubs sequences of the comprise compresent oligonucleotides, all of which are used in the exemplification comprises the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                        the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 18269; 2537pp + CD ROM; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length cDNAs -
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274 AA;
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1 T, Wakamatsu
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A, Nagai K,
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AAG66956
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AAG66956 standard; Protein;
                                                                                                                245 lhaleqgglraatmsaveaatcrakel 271
                                                                                                                                                            236 LHFLESGGFRSLLINAVEASCIRTREL 262
                                                                                                                                                                                                         185 cafsealaegavkmgmpsslahriaaqtllgtakmllhegqhpaqlrsdvctpggttlyg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 vgfvgagrmagaiaqgliragkveaghilasaptdrnlchfqal---gcrtthsngevlq 67
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scllvifatkphvlpavlaevapvvttehilvsvaagvslstleell---ppntrvlrvl 124
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45.3%; Pred. No. 3.9e-49;
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AAG66956;

22-OCT-2001 (first entry)

Human dihydropyrrole-5-carboxylate reductase 30 polypeptide.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel polypeptide, human dihydropyrrole-5-carboxylate reductase 30, polynucleotides encoding this polypeptide and a DNA recombination process to produce the polypeptide. The polypeptide is useful for treating various diseases, such as malignant tumours, nosohaemia, HIV infection, immunological such as and inflammatory diseases. The invention also provides an antibody against the polypeptide. The present sequence is the polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human dihydropyrrole-5-carboxylate reductase 30 as one new kind of polypeptide and polynucleotides encoding this polypeptide -
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                                                                                                                                                                                                          AAG06978 standard; Protein; 276 AA
                         Arabidopsis thaliana protein fragment SEQ ID NO: 3954
                                                                                        17-OCT-2000 (first entry)
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245 || haleggglraatmsaveaatcrakel 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pnlpcvvqegaivmargrhvgssetkllqhlleacgrceevpeayvdihtglsgsgvafv 184
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Pred. No. 8.2e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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nilarity 42.5%;
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                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana
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mapping; gene expression control; promoter;
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13-OCT-1999;
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   PHIIPFILDEIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMTNTPVVVQEG 127
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  7; Gaps
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   RESULT 11
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   The invention relates to a method for producing L-pipecolic acid. The method comprises reducing delta-1-piperidine-6-carboxylic acid with pyrrolidine-5-carboxylate reductase. A recombinant Escherichia coli or coryneform bacterium that can express a gene encoding lysine-6-aminotransferase is cultured in an L-lysine-containing medium in order to produce L-pipecolic acid. L-pipecolic acid may be used as a pharmaceutical raw material. The process is efficient, and can be retained. The present sequence is the Escherichia coli product can be retained. The present sequence is the Escherichia coli proc
  Sequence
   polypeptide. The gene encoding this protein may be used
  Disclosure; Page 31-33; 54pp; Japanese.
  Producing L-pipecolic acid for use as a pharmaceutical raw material, comprises reducing delta-1-piperidine-6-carboxylic acid with pyrrolidine-5-carboxylate reductase particularly in recombinant
   N-PSDB; AAH48471
  Fujii T,
  WPI; 2001-418288/44.
  22-DEC-2000; 2000WO-JP09137.
  (SAOC ) MERCIAN CORP.
  L-pipecolic acid production; delta-1-piperidine-6-carboxylic acid; pyrrolidine-5-carboxylate reductase; lysine-6-aminotransferase;
                 59
  05-JUL-2001.
  WO200148216-A1
   Escherichia coli
  Escherichia coli proC polypeptide.
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  3 VGFIGAGQLAYRFTAAGILSAHKIIASSPEMNLPT---VSALR-KMGVNLTRSNKETVKH 58
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   237 atlmnavvaaakrsrel 253
SDVLFLAVKPHIIPFILDBIGADVQARHIVVSCAAGVTISSVEKKLMAFQPAPKVIRCMT 118
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64 adiifaavkpgimikvlseitsslnkdslvvsiaagvtldglar---alghdrk11ramp 120

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XX AAGG
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  protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
  Arabidopsis thaliana protein fragment SEQ ID NO: 3956.
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   17-OCT-2000 (first entry)
   06-SEP-2000.
   EP1033405-A2
  Arabidopsis thaliana.
  241 rvleekgfraavieam-----tkcmeksekls 267
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99US-0147493.
99US-0147935.
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23.7%; Score 372; DB 21; 52.7%; Pred. No. 8.7e-32; tive 23; Mismatches 45;
   60981
                  Length 151;
 Indels
 2
Gaps
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  δÃ
   В
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  Qy
                                 sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification, but was obtained in electronic format directly from the specification, but was obtained in electronic format directly from the
  16-DEC-1999;
07-APR-2000;
03-AUG-2000;
Sequence
   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
   WPI; 2001-376931/40.
N-PSDB; AAH65425.
   The present
   Claim 17; SEQ ID NO: 3960; 246pp + Sequence Listing; English.
  Nakagawa S,
Tateishi N,
  organic acid synthesis.
   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
   18-DEC-2000; 2000EP-0127688
  Corynebacterium
  26-SEP-2001 (first entry)
  (KYOW ) KYOWA HAKKO KOGYO KK
  20-JUN-2001.
   AAG90206;
   AAG90206 standard;
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  glutamicum
  13
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                         Patent Office.
 270
  invention provides a number of nucleotide and protein
  ; 99JP-0377484.
; 2000JP-0159162.
; 2000JP-0280988.
  Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
   protein fragment SEQ
  glutamicum
   Protein;
   270
  Ħ
  <u>х</u>
о:
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   176
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  These
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Query Match Best Local Similarity

23.6%;

Score 370; Pred. No.

3.5e-31;

Length 270;

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  Db
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   Qy
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   Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
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   04-JAN-2001
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   23-JUN-2000;
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   -JUL-1999
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   sgsspaylflvtealieagvnlglpratakklavasfegaatmmketgkepselragvss
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  (first entry)
   2000WO-IB00923
   99DE-1031419.
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ОУ ОУ ОУ ОУ

110

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109 115

53

Matches

93;

Conservative

56;

Mismatches

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Indels

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09-JUL-1999;
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03-SEP-1999;
03-SEP-1999;
   Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases.
  03-SEP-1999;
03-SEP-1999;
  14-JUL-1999;
   in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
   AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals
  Claim 20; Page 589-590; 1737pp; English.
   N-PSDB; AAF71901
  31-AUG-1999;
   31-AUG-1999;
  14-JUL-1999;
   Sequence
   Pompejus M,
  (BADI ) BASF AG.
  compounds,
Local Similarity
   2001-137957/14.
   vitamins, cofactors, polyketides and
  270 AA;
   99DE-1042079.

99DE-1042086.

99DE-1042087.

99DE-1042087.

99DE-1042088.

99DE-1042095.

99DE-1042129.

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   Haberhauer
   <u>ن</u>
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Query Match
Best Local
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  AAG81123
  This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an organism
  Sequence
   Disclosure; Page 161; 207pp; English.
   Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
  Eisenberg D,
   N-PSDB; AAH51974.
   WPI; 2001-329193/34.
54 lvtsaadavenatfvvvavkpadvepviadlanataaaendsaegvfvtvvagitiayfe 113
                              48 LTRSNKETVKHSDVLFLAVKP-HIIPFILDEIGADV-----QARHIVVSCAAGVTISSVE 101
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   01-FEB-2000; 2000US-0179531
  12-NOV-1999;
12-NOV-1999;
  13-NOV-2000; 2000WO-US31152
   17-MAY-2001.
   Drug target; growth; organism viability; characterisation
  Mycobacterium tuberculosis potential drug target protein SEQ ID 174
   04-SEP-2001 (first entry)
  WO200135317-A1.
   Mycobacterium tuberculosis.
   AAG81123 standard; Protein; 295 AA.
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   233 pagttvaaireleesgirgafyraagacadrseel 267
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  228 PGGATIHALHFLESGGFRSLLINAVEASCIRTREL 262
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В

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   Дb
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  162 LIDAVTGLSGSGPAYAFMALDA--DGGVKMGLPRRLAIQLGAQALLGAAKMLLDSEQH-- 217
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